

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 16:27:29 ; Search time 121.018 Seconds  
(without alignments)  
281.578 Million cell updates/sec

Title: US-09-910-483-7

Perfect score: 566

Sequence: 1 DIQMTQSPSSLSASVGRVT.....QQSNMPTFGQGTKEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*  
15: SP\_virus:\*  
16: SP\_bacteriap:\*  
17: SP\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	476	84.1	108	Q9UL77	Q9UL77 homo sapien
2	465.5	82.2	107	Q96SA9	Q96SA9 homo sapien
3	457	80.7	236	Q7Z3Y4	Q7Z3Y4 homo sapien
4	456	80.6	108	Q9UL70	Q9UL70 homo sapien
5	448.5	79.2	107	Q9UL81	Q9UL81 homo sapien
6	434	76.7	234	Q7Z473	Q7Z473 homo sapien
7	433	76.5	108	Q9UL79	Q9UL79 homo sapien
8	421	74.4	108	Q9UL83	Q9UL83 homo sapien
9	420	74.2	116	Q96PF6	Q96PF6 homo sapien
10	407.5	72.0	109	Q9UL85	Q9UL85 homo sapien
11	405	71.6	234	Q91WF8	Q91WF8 mus musculu
12	405	71.6	234	Q8R062	Q8R062 mus musculu
13	401	70.8	108	Q8V1J0	Q8V1J0 mus musculu
14	396	70.0	233	Q91WS9	Q91WS9 mus musculu
15	393	69.4	109	Q920E6	Q920E6 mus musculu
16	392	69.3	214	Q9RIAS	Q9RIAS mus musculu

17	390	68.9	236	11	Q7TWK3	Q7TWK3 mus musculu
18	389	68.7	238	11	Q9OYF0	Q9OYF0 mus musculu
19	387	68.4	234	11	Q8VCP0	Q8VCP0 mus musculu
20	386.5	68.3	109	4	Q9UL78	Q9UL78 homo sapien
21	384	67.8	236	11	Q7TS98	Q7TS98 mus musculu
22	383	67.7	107	11	Q9UL84	Q9UL84 mus musculu
23	378	66.8	111	11	Q920E9	Q920E9 mus musculu
24	374.5	66.2	114	11	Q8K1F1	Q8K1F1 mus musculu
25	368.5	65.1	109	4	Q9UL86	Q9UL86 homo sapien
26	367.5	64.9	112	11	Q8K1F3	Q8K1F3 mus musculu
27	366.5	64.8	112	11	Q8K1F2	Q8K1F2 mus musculu
28	363.5	64.2	243	11	Q7TQM2	Q7TQM2 mus musculu
29	362	64.0	127	11	Q92S59	Q92S59 mus musculu
30	361	63.8	111	11	Q8L1U6	Q8L1U6 mus musculu
31	360.5	63.7	134	11	Q8VDD0	Q8VDD0 mus musculu
32	354	62.5	99	11	Q9UL74	Q9UL74 mus musculu
33	352.5	62.3	238	11	Q9NM37	Q9NM37 mus musculu
34	350	61.8	131	11	Q8L1C3	Q8L1C3 mus musculu
35	348.5	61.6	238	11	Q8VCI6	Q8VCI6 mus musculu
36	345	61.0	107	11	Q9ERZ9	Q9ERZ9 mus musculu
37	343	60.6	101	11	Q9JL78	Q9JL78 mus musculu
38	342.5	60.5	106	5	Q9UL10	Q9UL10 echiosoma
39	342.5	60.5	239	11	Q8VCS5	Q8VCS5 mus musculu
40	341	60.2	237	13	Q7S236	Q7S236 xenopus lae
41	339.5	60.0	235	11	Q7TWK0	Q7TWK0 mus musculu
42	335.5	59.3	239	4	Q8NEK0	Q8NEK0 homo sapien
43	333.5	58.9	235	11	Q9JW12	Q9JW12 mus musculu
44	332.5	58.7	112	11	Q8K1F0	Q8K1F0 mus musculu
45	330.5	58.4	239	4	Q8TCD0	Q8TCD0 homo sapien

## ALIGNMENTS

RESULT 1  
ID Q9UL77 PRELIMINARY; PRT; 108 AA.  
AC Q9UL77;  
DT 01-MAY-2000 (TREMURel. 13, Created)  
DT 01-MAY-2000 (TREMURel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMURel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
DS (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88271139; Pubmed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
DR EMBL: AF035037; AAD56273.1; -.  
DR PIR: B49047; B49047.  
DR PIR: S34083; S34083.  
DR HSP; P01607; IREI.  
DR InterPro: IPR007110; Ig\_1like.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IGV\_1.  
DR PROSITE: PS50835; IG\_LIKE; 1.  
FT NON TER 1  
FT TER 108  
SQ SEQUENCE 108 AA; 11738 MW; C06681716CAD16F3 CRC64;  
Query Match 84.1%; Score 476; DB 4; Length 108;  
Best Local Similarity 88.0%; Pred. No. 6.7e-46;  
Matches 95; Conservative 4; Mismatches 9; Indels 0; Gaps 0;  
OY 1 DIQMTQSPSSLSASVGRVTITCRASQISNNLHWYQOKPKAKLIIYHSAQSISGVPS 60

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Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQSSISYLNMYQOKPKKAPKLIYAASLSQSGVPS 60
QY 61 RFSGSGSTDTFTLTISLQPEDPATYTCQGSNSMPYTFGGGTVEIKR 108
Db 61 RFSGSGSTDTFTLTISLQPEDPATYTCQGSNSMPYTFGGGTVEIKR 108

RESULT 2
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes."
RT J. Immunol. 161:2020-2031(1998).
RL EMBL; U96396; AAB6785.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B57F16 CRC64;

Query Match 82.2%; Score 465.5; DB 4; Length 107;
Best Local Similarity 88.9%; Pred. No. 1e-44;
Matches 96; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQSSISYLNMYQOKPKKAPKLIYAASLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQSSISYLNMYQOKPKKAPKLIYAASLSQSGVPS 60

QY 61 RFSGSGSTDTFTLTISLQPEDPATYTCQGSNSMPYTFGGGTVEIKR 108
Db 61 RFSGSGSTDTFTLTISLQPEDPATYTCQGSNSMPYTFGGGTVEIKR 107

RESULT 3
Q7Z3Y4 PRELIMINARY; PRT; 236 AA.
ID Q7Z3Y4
AC Q7Z3Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaez T.E.,
RA Brownstein M.J., Ueda T.B., Tohyuki S., Granger C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez M.I., Skalka U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AA05332.1; -.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7BFPE4ED23084BC6 CRC64;

Query Match 80.7%; Score 457; DB 4; Length 236;
Best Local Similarity 84.3%; Pred. No. 2.6e-43;
Matches 91; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQSSISYLNMYQOKPKKAPKLIYAASLSQSGVPS 60
Db 23 DIQMTQSPSSLSASVGDRTVITTCRASQSSISYLNMYQOKPKKAPKLIYAASLSQSGVPS 82

QY 61 RFSGSGSTDTFTLTISLQPEDPATYTCQGSNSMPYTFGGGTVEIKR 108
Db 83 RFSGSGSTDTFTLTISLQPEDPATYTCQGSNSMPYTFGGGTVEIKR 130

RESULT 4
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; IRI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT SEQUENCE 108 AA; 11633 MW; B7BED3E41FCCA37 CRC64;

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Query Match 80.6%; Score 456; DB 4; Length 108;  
Best Local Similarity 85.2%; Pred. No. 1.2e-43;  
Matches 92; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIQWTPSSISASVGDRTTTCRASQISNNLHWYQKPKAKLLIYHASQISGVPS 60  
DB 1 DIQWTPSSISASVGDRTTTCRASQISNNLHWYQKPKAKLLIYHASQISGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDPATYTCQGSNSMPYFGQTKVEIKR 108  
DB 61 RFGSGSGTDFTLTISLQPEDPATYTCQGSNSMPYFGQTKVEIKR 108

RESULT 5  
Q9UL81 PRELIMINARY; PRT; 107 AA.

AC Q9UL81;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98271139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035033; AAD56269.1; -.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Iq-1like.  
DR InterPro; IPR003596; Iq\_v.  
DR Pfam; PF00047; Iq; 1.  
DR SMART; SM00406; Iq; 1.  
DR PROSITE; PSS00835; Iq\_LIKE; 1.  
FT NON\_TER 1  
FT 107  
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 79.2%; Score 448.5; DB 4; Length 107;  
Best Local Similarity 85.2%; Pred. No. 8.4e-43;  
Matches 92; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 1 DIQWTPSSISASVGDRTTTCRASQISNNLHWYQKPKAKLLIYHASQISGVPS 60  
DB 1 DIQWTPSSISASVGDRTTTCRASQISNNLHWYQKPKAKLLIYHASQISGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDPATYTCQGSNSMPYFGQTKVEIKR 108  
DB 61 RFGSGSGTDFTLTISLQPEDPATYTCQGSNSMPYFGQTKVEIKR 108

RESULT 6  
Q7Z473 PRELIMINARY; PRT; 234 AA.

AC Q7Z473;  
DT 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;

RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Bluetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,  
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Tothiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smalls D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RX Submitted (JUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC056256; AAH56256.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259AB51BC0F CRC64;

Query Match 76.7%; Score 434; DB 4; Length 234;  
Best Local Similarity 80.4%; Pred. No. 1e-40;  
Matches 86; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 2 IQWTPSSISASVGDRTTTCRASQISNNLHWYQKPKAKLLIYHASQISGVPSR 61  
DB 22 IQWTPSSISASVGDRTTTCRASQISNNLHWYQKPKAKLLIYHASQISGVPSR 81

QY 62 RFGSGSGTDFTLTISLQPEDPATYTCQGSNSMPYFGQTKVEIKR 108  
DB 82 RFGSGSGTDFTLTISLQPEDPATYTCQGSNSMPYFGQTKVEIKR 128

RESULT 7  
Q9UL79 PRELIMINARY; PRT; 108 AA.

AC Q9UL79;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98271139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035035; AAD56271.1; -.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Iq-1like.  
DR InterPro; IPR003596; Iq\_v.  
DR Pfam; PF00047; Iq; 1.  
DR SMART; SM00406; Iq; 1.  
DR PROSITE; PSS00835; Iq\_LIKE; 1.  
FT NON\_TER 1  
FT 108

```

FT  NON TER      108      108
SQ  SEQUENCE     108 AA; 11787 MW;  DB5845F19724FB4E CRC64;

Query Match
Best Local Similarity 76.5%; Score 433; DB 4; Length 108;
Matches 88; Conservative 4; Pred. No. 4.8e-41;
Indels 0; Gaps 0;

QY  1 DIOMTQSPSSLSASVGDRTVITTCRASQSIENNLMHWYQOKGKAPKLLIYHASQISGVPS 60
DB  1 DIOMTQSPSSLSASVGDRTVITTCRASQSIENNLMHWYQOKGKAPKLLIYHASQISGVPS 60
QY  61 RFGSGSGGDTFTLTISLQPEDPATYTCQGSNSMPYTFGQGTVEIKR 108
DB  61 RFGSGSGGDTFTLTISLQPEDPATYTCQGSNSMPYTFGQGTVEIKR 108

RESULT 8
QY  Q9UL83      PRELIMINARY; PRT; 108 AA.
AC  Q9UL83;
DT  01-MAY-2000 (TReMBLrel. 13, Created)
DT  01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT  01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE  Myosin-reactive immunoglobulin light chain variable region
    (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=98277139; PubMed=9614934;
RA  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA  Young D.C.;
RT  "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT  fetus."
RL  Clin. Immunol. Immunopathol. 87:184-192(1998).
DR  EMBL; AF035031; AAD56267.1; -.
DR  PIR; B30609; B30609.
DR  PIR; C30609; C30609.
DR  PIR; D30609; D30609.
DR  PIR; S34098; S34098.
DR  PIR; S34099; S34099.
DR  HSSP; P80362; 1MTL.
DR  InterPro; IPR007110; Ig_1like.
DR  InterPro; IPR003596; Ig_v.
DR  SMART; SM00406; IGV_1.
DR  SMART; SM00406; IGV_1.
DR  PROSITE; PSS0835; IG_LIKE; 1.
FT  NON_TER      108      108
SQ  SEQUENCE     108 AA; 11834 MW;  9F9C5A922EBA96EBA CRC64;

Query Match
Best Local Similarity 74.4%; Score 421; DB 4; Length 108;
Matches 77; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY  1 DIOMTQSPSSLSASVGDRTVITTCRASQSIENNLMHWYQOKGKAPKLLIYHASQISGVPS 60
DB  1 EIMWTQSPALSLVSPGRATLSCRASQSVSNLAWYQOKGQAPRLIILYASRATGIRA 60
QY  61 RFGSGSGGDTFTLTISLQPEDPATYTCQGSNSMPYTFGQGTVEIKR 108
DB  61 RFGSGSGGDTFTLTISLQPEDPATYTCQGSNSMPYTFGQGTVEIKR 108

RESULT 9
QY  Q96PF6      PRELIMINARY; PRT; 116 AA.
AC  Q96PF6;
DT  01-DEC-2001 (TReMBLrel. 19, Created)
DT  01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT  01-OCT-2003 (TReMBLrel. 25, Last annotation update)

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```

DE  Kappa 1 light chain variable region (Fragment).
GN  GNKL.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21361171; PubMed=11468171;
RA  Clemenso R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RA  "The tropism of organ involvement in primary systemic amyloidosis:
RT  contributions of Ig VL(D) germ line gene use and clonal plasma cell
RT  burden."
RL  Blood 98:714-720 (2001).
DR  EMBL; AF361758; AAK51465.1; -.
DR  InterPro; IPR007110; Ig_1like.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig_1.
DR  SMART; SM00406; IGV_1.
DR  PROSITE; PSS0835; IG_LIKE; 1.
FT  NON_TER      116      116
SQ  SEQUENCE     116 AA; 12735 MW;  E796FC2217BFCF57 CRC64;

Query Match
Best Local Similarity 74.2%; Score 420; DB 4; Length 116;
Matches 80; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY  1 DIOMTQSPSSLSASVGDRTVITTCRASQSIENNLMHWYQOKGKAPKLLIYHASQISGVPS 60
DB  1 DIOMTQSPSSLSASVGDRTVITTCRASQSIENNLMHWYQOKGKAPKLLIYHASQISGVPS 60
QY  61 RFGSGSGGDTFTLTISLQPEDPATYTCQGSNSMPYTFGQGTVEIKR 108
DB  61 RFGSGSGGDTFTLTISLQPEDPATYTCQGSNSMPYTFGQGTVEIKR 108

RESULT 10
QY  Q9UL85      PRELIMINARY; PRT; 109 AA.
AC  Q9UL85;
DT  01-MAY-2000 (TReMBLrel. 13, Created)
DT  01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT  01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE  Myosin-reactive immunoglobulin kappa chain variable region
    (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=98277139; PubMed=9614934;
RA  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA  Young D.C.;
RT  "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT  fetus."
RL  Clin. Immunol. Immunopathol. 87:184-192(1998).
DR  EMBL; AF035029; AAD56265.1; -.
DR  PIR; D30609; D30609.
DR  HSSP; P80362; 1MTL.
DR  InterPro; IPR007110; Ig_1like.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig_1.
DR  SMART; SM00406; IGV_1.
DR  SMART; SM00406; IGV_1.
DR  PROSITE; PSS0835; IG_LIKE; 1.
FT  NON_TER      109      109
SQ  SEQUENCE     109 AA; 11761 MW;  FB1E43E7C7AFACCC CRC64;

Query Match
Best Local Similarity 72.0%; Score 407.5; DB 4; Length 109;
Matches 79; Conservative 14; Mismatches 15; Indels 1; Gaps 1;

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AC Q91WS9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon;  
RA Strausberg R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC013496; AAI13496.1; -  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR Pfam: PF00047; Ig; 2.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS00835; IG\_LIKE; 2.  
DR PROSITE: PS00290; IG\_MHC; 1.  
KM Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;  
  
Query Match 70.0%; Score 396; DB 11; Length 233;  
Best Local Similarity 71.3%; Pred. No. 1.9e-36;  
Matches 77; Conservative 12; Mismatches 19; Indels 0; Gaps 0;  
  
QY 1 DIQMTQSPSSLSASVDGRTVITCRASQISNNLHWYQOKPKAKLLIYHASQISGVPS 60  
Db 20 DIQMTQSPSSLSASVDGRTVITCRASQISNNLHWYQOKPKAKLLIYHASQISGVPS 60  
QY 61 RFGSGSGTDFTLTISLSLOPEDPATYCCQSNMPTFGQTKVEIKR 108  
Db 80 RFGSGSGTDYSLTISNLEPEDIATYCCQRYRLPWTFGGTLKLEIKR 127  
  
RESULT 15  
Q920E6 PRELIMINARY; PRT; 109 AA.  
AC Q920E6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Pterin-mimicking anti-idiotope kappa chain variable region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Atkin J.D., Iape A., Jennings I.G., Horatits O., Cotton R.G.H.;  
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF307938; AAL09422.1; -  
DR PIR: S19112; S19112.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS00835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 109  
SQ SEQUENCE 109 AA; 11943 MW; DAD3F98E05DD1501 CRC64;  
  
Query Match 69.4%; Score 393; DB 11; Length 109;  
Best Local Similarity 70.4%; Pred. No. 1.6e-36;  
Matches 76; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRTVITCRASQISNNLHWYQOKPKAKLLIYHASQISGVPS 60  
Db 1 DIQMTQSPSSLSASVDGRTVITCRASQISNNLHWYQOKPKAKLLIYHASQISGVPS 60  
QY 61 RFGSGSGTDFTLTISLSLOPEDPATYCCQSNMPTFGQTKVEIKR 108  
Db 61 RFGSGSGTDYSLKINSLSLOPEDGSGYCCHFWSMPTFGGTLKLEIKR 108  
  
Search completed: May 13, 2004, 17:01:48  
Job time : 122.018 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 16:27:29 ; Search time 129,982 Seconds  
(without alignments)  
281.578 Million cell updates/sec

Title: US-09-910-483-5  
Perfect score: 617  
Sequence: 1 EVGLVESGGGLVPGGSLRL.....TAGSYWPAWYGGQGLTVTVSS 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP archaea: \*  
2: SP bacteria: \*  
3: SP fungi: \*  
4: SP human: \*  
5: SP invertebrate: \*  
6: SP mammal: \*  
7: SP mhc: \*  
8: SP organelle: \*  
9: SP phage: \*  
10: SP plant: \*  
11: SP rodent: \*  
12: SP virus: \*  
13: SP vertebrate: \*  
14: SP unclassified: \*  
15: SP virus: \*  
16: SP bacteriap: \*  
17: SP archaeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	441.5	71.6	113	4 Q9UL90	Q9UL90 homo sapien
2	435.5	70.6	116	4 Q9UL93	Q9UL93 homo sapien
3	435.5	70.6	597	4 Q96BB9	Q96BB9 homo sapien
4	427	69.2	118	4 Q9UL72	Q9UL72 homo sapien
5	427	69.2	613	4 Q8WUK1	Q8WUK1 homo sapien
6	421	68.2	122	4 Q9UL84	Q9UL84 homo sapien
7	419.5	68.0	121	4 Q9UL71	Q9UL71 homo sapien
8	419	67.9	573	4 Q8WU38	Q8WU38 homo sapien
9	417	67.6	112	4 Q9HCC1	Q9HCC1 homo sapien
10	415	67.3	118	4 Q9UL91	Q9UL91 homo sapien
11	415	66.4	494	4 Q96K68	Q96K68 homo sapien
12	409.5	66.4	131	4 Q9UL88	Q9UL88 homo sapien
13	409.5	66.4	499	4 Q8NSK4	Q8NSK4 homo sapien
14	406	65.8	473	11 Q91205	Q91205 mus musculi
15	403.5	65.4	487	11 Q80217	Q80217 mus musculi
16	400.5	64.9	493	4 Q8NCL6	Q8NCL6 homo sapien

17	399.5	64.7	119	11 Q920E7	Q920E7 mus musculi
18	398	64.5	147	4 Q9Y509	Q9Y509 homo sapien
19	395	64.0	469	11 Q8R3V9	Q8R3V9 mus musculi
20	394.5	63.9	521	4 Q8N4Y9	Q8N4Y9 homo sapien
21	393.5	63.8	470	4 Q7Z5M1	Q7Z5M1 homo sapien
22	390.5	63.3	480	11 Q91XE1	Q91XE1 mus musculi
23	385.5	62.5	479	11 Q91WP5	Q91WP5 mus musculi
24	378	61.3	487	11 Q99KA4	Q99KA4 mus musculi
25	375.5	60.9	473	11 Q9DBL4	Q9DBL4 mus musculi
26	372	60.3	479	11 Q7TMC4	Q7TMC4 mus musculi
27	371	60.1	298	11 Q9QYF0	Q9QYF0 mus musculi
28	368	59.6	95	4 Q9ULB6	Q9ULB6 homo sapien
29	363.5	58.9	468	11 Q99L31	Q99L31 mus musculi
30	360.5	58.4	486	11 Q91Z07	Q91Z07 mus musculi
31	360	58.3	484	11 Q8VBA0	Q8VBA0 mus musculi
32	356.5	57.8	109	11 Q9ULB5	Q9ULB5 mus musculi
33	352	57.1	124	4 Q9UL92	Q9UL92 homo sapien
34	345	55.9	437	11 Q9R1A4	Q9R1A4 mus sapien
35	343.5	55.7	119	4 Q9UL94	Q9UL94 homo sapien
36	341.5	55.3	482	4 Q7Z351	Q7Z351 homo sapien
37	341.5	55.3	614	11 Q7TMT6	Q7TMT6 mus musculi
38	339.5	55.0	481	11 Q91WT1	Q91WT1 mus musculi
39	338.5	54.9	104	4 Q9ULB7	Q9ULB7 homo sapien
40	337.5	54.7	125	4 Q9UL95	Q9UL95 homo sapien
41	335.5	54.4	117	11 Q9QXF0	Q9QXF0 mus musculi
42	335	54.3	124	6 Q9NOM4	Q9NOM4 oryctolagus
43	333	54.0	463	11 Q99LC4	Q99LC4 mus musculi
44	332.5	53.9	146	11 Q924R8	Q924R8 mus musculi
45	332	53.8	124	6 Q9NOM6	Q9NOM6 oryctolagus

## ALIGNMENTS

RESULT 1  
Q9UL90 PRELIMINARY; PRT; 113 AA.  
ID Q9UL90  
AC Q9UL90;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98271139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL: AF035024; AAD56260.1; -.  
DR HSRP: P01772; 2F84.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGv; 1.  
DR PROSITE: PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 113  
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;  
Query Match 71.6%; Score 441.5; DB 4; Length 113;  
Best Local Similarity 76.7%; Pred. No. 3.9e-38;  
Matches 89; Conservative 3; Mismatches 21; Indels 3; Gaps 1;  
QY 1 EVGLVESGGGLVPGGSLRLSCAASGFTFSSYGMHWRAQPGKGLVAVIRYDGSNKY 60  
Db 1 EVGLVESGGGVVPGGSLRLSCAASGFTFSSYGMHWRAQPGKGLVAVIRYDGSNKY 60





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AC Q8WUJ1;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AA020240.1; -
DR PIR; P0120; P0120.
DR PIR; S15590; S15590.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG-LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KM Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C75950671E315 CRC64;

Query Match 69.2%; Score 427; DB 4; Length 613;
Best Local Similarity 71.3%; Pred. No. 1,le-35;
Matches 87; Conservative 5; Mismatches 22; Indels 8; Gaps 2;

QY 1 EVOLVESGGGVGGGSLRLSCAAGFNIKDTYIHWRAQPGKLEWVARIDPANDNTIY 60
DB 20 QVQLVESGGGVQVQGRSLRLSCAAGFIFSSYGMHWRAQPGKLEWVAIVSYGSKNTY 79
QY 61 ADSVKGKFTTSSDSSKNTAYLQNNLSLRADTAIVYCTASGYW-----FAYWGQGLTVTV 114
DB 80 ADSVKGKFTTSSDSSKNTAYLQNNLSLRADTAIVYCTASGYW-----FAYWGQGLTVTV 137
QY 115 SS 116
DB 138 SS 139

RESULT 6
Q9UL84 PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56266.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 1
FT SEQUENCE 121 AA; 13154 MW; 2F045CFA5D50736 CRC64;

Query Match 68.0%; Score 419.5; DB 4; Length 121;
Best Local Similarity 69.4%; Pred. No. 8.3e-36;
Matches 84; Conservative 8; Mismatches 24; Indels 5; Gaps 1;

QY 1 EVOLVESGGGVGGGSLRLSCAAGFNIKDTYIHWRAQPGKLEWVARIDPANDNTIY 60
DB 1 EVOLVESGGGVQVQGRSLRLSCAAGFIFSSYGMHWRAQPGKLEWVAIVSYGSKNTY 79
QY 61 ADSVKGKFTTSSDSSKNTAYLQNNLSLRADTAIVYCTASGYW-----WGQGLTVTVS 115
DB 61 ADSVKGKFTTSSDSSKNTAYLQNNLSLRADTAIVYCTASGYW-----WGQGLTVTVS 120
QY 116 S 116
DB 121 S 121

RESULT 8
Q8WU38 PRELIMINARY; PRT; 573 AA.
AC Q8WU38;

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FT NON_TER 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 68.2%; Score 421; DB 4; Length 122;
Best Local Similarity 70.5%; Pred. No. 5.8e-36;
Matches 86; Conservative 5; Mismatches 25; Indels 6; Gaps 1;

QY 1 EVOLVESGGGVGGGSLRLSCAAGFNIKDTYIHWRAQPGKLEWVARIDPANDNTIY 60
DB 1 EVOLVESGGGVQVQGRSLRLSCAAGFIFSSYGMHWRAQPGKLEWVAIVSYGSKNTY 79
QY 61 ADSVKGKFTTSSDSSKNTAYLQNNLSLRADTAIVYCTASGYW-----GYWFAWGQGLTVTV 114
DB 61 ADSVKGKFTTSSDSSKNTAYLQNNLSLRADTAIVYCTASGYW-----GYWFAWGQGLTVTV 120
QY 115 SS 116
DB 121 SS 122

RESULT 7
Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 1
FT SEQUENCE 121 AA; 13154 MW; 2F045CFA5D50736 CRC64;

Query Match 68.0%; Score 419.5; DB 4; Length 121;
Best Local Similarity 69.4%; Pred. No. 8.3e-36;
Matches 84; Conservative 8; Mismatches 24; Indels 5; Gaps 1;

QY 1 EVOLVESGGGVGGGSLRLSCAAGFNIKDTYIHWRAQPGKLEWVARIDPANDNTIY 60
DB 1 EVOLVESGGGVQVQGRSLRLSCAAGFIFSSYGMHWRAQPGKLEWVAIVSYGSKNTY 79
QY 61 ADSVKGKFTTSSDSSKNTAYLQNNLSLRADTAIVYCTASGYW-----WGQGLTVTVS 115
DB 61 ADSVKGKFTTSSDSSKNTAYLQNNLSLRADTAIVYCTASGYW-----WGQGLTVTVS 120
QY 116 S 116
DB 121 S 121

RESULT 8
Q8WU38 PRELIMINARY; PRT; 573 AA.
AC Q8WU38;

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DT 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA Strausberg R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC021276; AAH21276.1; -  
 DR PIR; S21205; S21205.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 573 AA; 62967 MW; PD072344033AC530 CRC64;

Query Match 67.9%; Score 419; DB 4; Length 573;  
 Best Local Similarity 69.4%; Pred. No. 6.9e-35;  
 Matches 86; Conservative 9; Mismatches 21; Indels 8; Gaps 2;

QY 1 EVOLVESGGGLVOPGSGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60  
 DB 20 EVOLVESGGGLVOPGSGSLRLSCAASGFTFDDYAMHWRAQAPGKLEWVSIGINNGSGTGY 79  
 QY 61 ADVSKGRFTISSDSDSKNTAYLQNSLRADTVAVYCT--ASGYWFAV-----WGCGTIV 112  
 DB 80 ADVSKGRFTISSDSDSKNTAYLQNSLRADTVAVYCAHGSGSYITGYGMDVWGCGTIV 139  
 QY 113 TVSS 116  
 DB 140 TVSS 143

RESULT 9  
 Q9HCC1 PRELIMINARY; PRT; 112 AA.  
 AC Q9HCC1;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, last annotation update)  
 DE Single chain Fv (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;  
 RT "An antibody fragment2A3 specific for native lysozyme: isolation from a  
 human synthetic phage display library and characterization.";  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB049915; BAB16829.1; -  
 DR HSP; P01772; 2F84.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 112  
 SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 67.6%; Score 417; DB 4; Length 112;  
 Best Local Similarity 72.3%; Pred. No. 1.4e-35;

Matches 81; Conservative 10; Mismatches 21; Indels 0; Gaps 0;  
 QY 1 EVOLVESGGGLVOPGSGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60  
 DB 1 EVOLVESGGGLVOPGSGSLRLSCAASGFTFDDYAMHWRAQAPGKLEWVSIGINNGSGTGY 60  
 QY 61 ADVSKGRFTISSDSDSKNTAYLQNSLRADTVAVYCT--ASGYWFAV-----WGCGTIV 112  
 DB 61 ADVSKGRFTISSDSDSKNTAYLQNSLRADTVAVYCAHGSGSYITGYGMDVWGCGTIV 112

RESULT 10  
 Q9UL91 PRELIMINARY; PRT; 118 AA.  
 AC Q9UL91;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region  
 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Werwe P.V., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
 DR EMBL; AF035023; AAD56259.1; -  
 DR PIR; S21205; S21205.  
 DR HSP; P01772; 2F84.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 118  
 SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 67.3%; Score 415; DB 4; Length 118;  
 Best Local Similarity 71.8%; Pred. No. 2.4e-35;  
 Matches 84; Conservative 7; Mismatches 24; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVOPGSGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60  
 DB 1 EVOLVESGGGLVOPGSGSLRLSCAASGFTFSSYSMMWVRQAPGKLEWVSISTITITTY 60  
 QY 61 ADVSKGRFTISSDSDSKNTAYLQNSLRADTVAVYCTA--SGYWFAVWGCGTIVTVS 115  
 DB 61 ADVSKGRFTISSDSDSKNTAYLQNSLRADTVAVYCARDSSEARDIWGCGTIVTVS 117

RESULT 11  
 Q96K68 PRELIMINARY; PRT; 494 AA.  
 AC Q96K68;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, last annotation update)  
 DE Hypothetical protein FL114473.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
 RA Nagatsuma M., Hosori T., Kaku Y., Kodaira H., Kondo Y., Sugawara M.,  
 RA Takahashi M., Chiba Y., Ichida S., Murakawa K., Ono Y., Takiguchi S.,  
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Maehuo Y.,  
 RA Nishimura K., Iwayanagi T.,  
 RT "MDO human cDNA sequencing project."  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK027379; BAB55072.1; -  
 DR PIR: S21205; S21205.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 4.  
 DR SMART: SM00406; Ig; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 494 AA; 53088 MW; 9A1D7A8B5AE4C0E CRC64;

Query Match 67.3%; Score 415; DB 4; Length 494;  
 Best Local Similarity 68.0%; Pred. No. 1.5e-34;  
 Matches 83; Conservative 11; Mismatches 22; Indels 6; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDTIY 60  
 DB 20 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDTIY 79  
 QY 61 ADVSKGRFTISDDSKNTAYLQNMSLRAEDTAVVYCT-----ASGYFAYWGQGLTVT 114  
 DB 80 RDSVKGKFTISRDAKNSLYLQNMSLRVDDTAVVYCARDCNGALICGFSPWGQGLTVT 139  
 QY 115 SS 116  
 DB 140 SS 141

RESULT 12  
 Q9UL88 PRELIMINARY; PRT; 131 AA.  
 AC Q9UL88;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9827139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M.,  
 RA Young D.C.,  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus."  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL: AF035026; AAD56262.1; -  
 DR PIR: S21205; S21205.  
 DR HSSP: P01810; 2FBJ.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; Ig; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 131  
 SQ SEQUENCE 131 AA; 14142 MW; 96E7D668537DEAD0 CRC64;

Query Match 66.4%; Score 409.5; DB 4; Length 131;  
 Best Local Similarity 64.9%; Pred. No. 1e-34;  
 Matches 85; Conservative 6; Mismatches 25; Indels 15; Gaps 2;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPAND--NT 58  
 DB 1 EVOLVESGGGLVOPGSLRLSCAASGFTFSKAMSWVRQAPGKLEWVGIRKKTGGCTT 60  
 QY 59 IYADVSKGRFTISDDSKNTAYLQNMSLRAEDTAVVYCT-----ASGYFAY 105  
 DB 61 DYAPVKGRLTISRDSKNTLYLRMSLKTEDTAVVYCTGITIIVITTSKRISFEY 120  
 QY 106 WGQGLTVTSS 116  
 DB 121 WGQGLTVTSS 131

RESULT 13  
 Q8NSK4 PRELIMINARY; PRT; 499 AA.  
 AC Q8NSK4;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RA Strauberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC032249; AAH32249.1; -  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig\_C1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 4.  
 DR SMART: SM00409; Ig; 4.  
 DR SMART: SM00407; IG\_C1; 2.  
 DR SMART: SM00406; Ig; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;

Query Match 66.4%; Score 409.5; DB 4; Length 499;  
 Best Local Similarity 63.8%; Pred. No. 5.6e-34;  
 Matches 81; Conservative 13; Mismatches 22; Indels 11; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDTIY 60  
 DB 20 EVOLVESGGGVPRPGSLRLSCATSGTFPDSGASVWRQAPGKLEWVSSINMNGSGTNY 79  
 QY 61 ADVSKGRFTISRDAKNSLYLQNMSLRVDDTAVVYCARDPKTCGSGSCGYMDWGK 109  
 DB 80 ADVSKGRFTISRDAKNSLYLQNMSLRVDDTAVVYCARDPKTCGSGSCGYMDWGK 139  
 QY 110 TVTVTSS 116  
 DB 140 TVTVTSS 146

RESULT 14  
 Q91Z05 PRELIMINARY; PRT; 473 AA.  
 AC Q91Z05;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN A004919.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Mus  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC010327; AAH0327.1; -  
DR MGD; MGI:2144567; AI0042919.  
DR GO; GO:0005489; F:electron transporter activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR000345; Cytochrome\_B8.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig\_f3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00190; CYTOCHROME\_C; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51946 MW; CP625F008932AF12 CR664;

Query Match	65.8%;	Score 406;	DB 11;	Length 473;
Best Local Similarity	67.2%;	Pred. No. 1.2e-33;		
Matches 80; Conservative	12;	Mismatches 23;	Indels 4;	Gaps 2;

QY EVOLVEGGGGIVDPGGSLRLTSCAASGENIDPTIHWWRQAPGGGLEVARIPDANTNTY 6  
| | | | | | | | | | | | | | | | :  
Db EVOLVEGGGGIVRPGGSRKLTSCAASGTFSDYGMHWWRQAPKGGLEVARVYINGSTITY 79

## RESULT 15

ID	ORG217	PRELIMINARY	PRT	487 AA.
AC	Q60217			
DT	01-JUN-2003	(TREMBLrel. 24, Created)		
DT	01-JUN-2003	(TREMBLrel. 24, Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DE	Hypothetical protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FVB/N; TISSUE=Colon;			
RA	Straussberg R.;			
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL, BC049143; AAH49143.1; -.			
DR	InterPro: IPR003599; IG.			
DR	InterPro: IPR007110; IG_1like.			
DR	InterPro: IPR003597; IG_c1.			
DR	InterPro: IPR003006; IG_MHC.			
DR	InterPro: IPR003596; IG_v.			
DR	Pfam: PF00047; Ig_3.			
DR	SMART: SM00409; IG; 3.			
DR	SMART: SM00407; IGC1; 3.			
DR	SMART: SM00406; IGV; 1.			
DR	PROSITE: PS50835; IG_LIKE; 4.			
DR	PROSITE: PS00290; IGMHC; 2.			
DR	Hypothetical protein.			
QO	SEQUENCE 487 AA; 53019 MW; 31F2C893900AD80 CRC64;			

Query Match	65.4%;	Score 403.5;	DB 11;	Length 487;
Best Local Similarity	64.2%;	Pred. No. 2.3e-33;		
Matches 79;	Conservative 17;	Mismatches 20;	Indels 7;	Gaps 2;

1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVRQAPEGKGLEWVARIDPAND--T 58

Db 20 EYLTJEBAGGGLVQPGSMKMLSCAASGFFFSNYMMNNWNRQSPKEKLEWVAIEIRLSNNYAT 79

QY 59 IYADSYKGFITSSDDSKATATLQMSLRADPDATVYCTASGY----WPAYMGGLVT 113

Db 80 HYAESYKGFITSRDSDKSSVYLQNNLRADPDGTGYCTRGGYDPNNYFEDWAGATTVT 139

QY 114 VSS 116

Db 140 VSS 142

Search completed: May 13, 2004, 17:01:47  
Job time : 131.982 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: May 13, 2004, 16:57:28 ; Search time 48.2143 Seconds

(without alignments)  
115.642 Million cell updates/sec

Title: US-09-910-483-7

Perfect score: 566  
Sequence: 1 DQMTQSPSSLSASVGRVT.....QQSNMPTFGQTKVEIKR 108Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/PCrus.COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	496	87.6	108	3 US-08-974-899-3	Sequence 3, Appli
2	491	86.7	107	2 US-07-934-373C-18	Sequence 18, Appl
3	491	86.7	107	3 US-08-437-642B-18	Sequence 18, Appl
4	491	86.7	107	4 US-08-146-206C-18	Sequence 18, Appl
5	491	86.7	107	4 US-08-648-067A-14	Sequence 14, Appl
6	491	86.7	107	4 US-09-705-686-18	Sequence 18, Appl
7	491	86.7	107	5 PCT-US93-07832-18	Sequence 18, Appl
8	491	86.7	109	3 US-07-934-373C-3	Sequence 3, Appli
9	491	86.7	109	3 US-08-437-642B-3	Sequence 3, Appli
10	491	86.7	109	4 US-08-146-206C-3	Sequence 3, Appli
11	491	86.7	109	4 US-09-705-686-3	Sequence 3, Appli
12	491	86.7	109	5 PCT-US93-07832-3	Sequence 3, Appli
13	489	86.4	109	3 US-09-157-370-3	Sequence 3, Appli
14	482	85.2	107	2 US-07-934-373C-17	Sequence 17, Appl
15	482	85.2	107	3 US-08-437-642B-17	Sequence 17, Appl
16	482	85.2	107	4 US-08-146-206C-17	Sequence 17, Appl
17	482	85.2	107	4 US-09-705-686-17	Sequence 17, Appl
18	482	85.2	107	5 PCT-US93-07832-17	Sequence 17, Appl
19	482	85.2	108	2 US-08-379-057-29	Sequence 29, Appl
20	482	85.2	109	3 US-07-934-373C-47	Sequence 47, Appl
21	482	85.2	109	3 US-08-437-642B-47	Sequence 47, Appl
22	482	85.2	214	2 US-07-934-373C-39	Sequence 39, Appl
23	482	85.2	214	2 US-07-934-373C-40	Sequence 40, Appl
24	482	85.2	214	2 US-08-788-880-11	Sequence 11, Appl
25	482	85.2	214	3 US-08-437-642B-39	Sequence 39, Appl
26	482	85.2	214	3 US-08-437-642B-40	Sequence 40, Appl
27	482	85.2	214	3 US-09-097-309-2	Sequence 2, Appli

28	482	85.2	214	3 US-09-097-171A-2	Sequence 2, Appli
29	482	85.2	214	4 US-09-460-587-2	Sequence 2, Appli
30	482	85.2	214	5 PCT-US93-07832-39	Sequence 39, Appl
31	482	85.2	214	5 PCT-US93-07832-40	Sequence 40, Appl
32	482	85.2	233	2 US-07-934-373C-25	Sequence 25, Appl
33	482	85.2	233	3 US-08-437-642B-25	Sequence 25, Appl
34	482	85.2	233	4 US-08-146-206C-25	Sequence 25, Appl
35	482	85.2	233	4 US-09-705-686-25	Sequence 25, Appl
36	482	85.2	233	5 PCT-US93-07832-25	Sequence 25, Appl
37	482	85.2	237	3 US-09-097-309-6	Sequence 6, Appli
38	482	85.2	237	3 US-09-097-171A-10	Sequence 10, Appl
39	482	85.2	237	3 US-09-422-712B-2	Sequence 2, Appli
40	482	85.2	237	3 US-09-607-756-2	Sequence 2, Appli
41	482	85.2	237	4 US-09-460-587-6	Sequence 6, Appli
42	481	85.0	108	2 US-08-378-939-32	Sequence 32, Appl
43	481	85.0	108	2 US-08-378-939-34	Sequence 34, Appl
44	481	85.0	108	4 US-09-025-769B-14	Sequence 14, Appl
45	480	84.8	111	1 US-08-137-117D-67	Sequence 67, Appl

## ALIGNMENTS

RESULT 1  
US-08-974-899-3

: Sequence 3, Application US/08974899

: Patent No. 6037454

: GENERAL INFORMATION:

: APPLICANT: Presta, Leonard G.

: APPLICANT: Jardiou, Paula M.

: TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

: NUMBER OF SEQUENCES: 24

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Genentech, Inc.

: STREET: 1 DNA Way

: CITY: South San Francisco

: STATE: California

: COUNTRY: USA

: ZIP: 94080

: COMPUTER READABLE FORM:

: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Winpatin (Genentech)

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/974,899

: FILING DATE:

: CLASSIFICATION: 536

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: 60/031971

: FILING DATE: 11/27/96

: ATTORNEY/AGENT INFORMATION:

: NAME: Lee, Wendy M.

: REGISTRATION NUMBER: 40,378

: REFERENCE/DOCKET NUMBER: P1014R1

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 650/225-1994

: TELEFAX: 650/952-9881

: INFORMATION FOR SEQ ID NO: 3:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 108 amino acids

: TYPE: Amino Acid

: TOPOLOGY: Linear

: US-08-974-899-3

Query Match 87.6%; Score 496; DB 3; Length 108;  
Best Local Similarity 91.7%; Pred. No. 1.1e-35;  
Matches 99; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DQMTQSPSSLSASVGRVTITCRASGISNNLHWYQKRGKPKLLIYASGISVPS 60  
Db 1 DQMTQSPSSLSASVGRVTITCRASGISNNLHWYQKRGKPKLLIYASGISVPS 60



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA: US/08/146,206C  
APPLICATION NUMBER: US/08/146,206C  
FILING DATE: 17-NO. 6407213-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-146-206C-18

Query Match 86.7%; Score 491; DB 4; Length 107;  
Best Local Similarity 91.6%; Pred. No. 2.8e-35;  
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCRAQGISNNLMHWYQOKPGKAPKLLIYHASQSIGVPS 60  
DB 1 DIQMTQSPSSLSASVGRVTITTCRAQGISNNLMHWYQOKPGKAPKLLIYHASQSIGVPS 60

QY 61 RFSSGSGTDFTLTISSLQPEDFATYYCOQNSWPTFGQGTKEIK 107  
DB 61 RFSSGSGTDFTLTISSLQPEDFATYYCOQNSLPTWFGQGTKEIK 107

RESULT 5  
US-09-648-067A-14  
Sequence 14, Application US/09648067A  
Patent No. 6627196  
GENERAL INFORMATION:  
APPLICANT: Baughman, Sharon A.  
APPLICANT: Shak Steven  
TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies  
FILE REFERENCE: P1775R1  
CURRENT APPLICATION NUMBER: US/09/648,067A  
CURRENT FILING DATE: 2000-08-25  
PRIOR APPLICATION NUMBER: US 60/151,018  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: US 60/213,822  
PRIOR FILING DATE: 2000-06-23  
NUMBER OF SEQ ID NOS: 15  
SEQ ID NO 14  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: VL consensus sequence  
US-09-648-067A-14

Query Match 86.7%; Score 491; DB 4; Length 107;  
Best Local Similarity 91.6%; Pred. No. 2.8e-35;  
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCRAQGISNNLMHWYQOKPGKAPKLLIYHASQSIGVPS 60  
DB 1 DIQMTQSPSSLSASVGRVTITTCRAQGISNNLMHWYQOKPGKAPKLLIYHASQSIGVPS 60

QY 61 RFSSGSGTDFTLTISSLQPEDFATYYCOQNSWPTFGQGTKEIK 107  
DB 61 RFSSGSGTDFTLTISSLQPEDFATYYCOQNSLPTWFGQGTKEIK 107

RESULT 6  
US-09-705-686-18  
Sequence 18, Application US/09705686  
Patent No. 663905  
GENERAL INFORMATION:  
APPLICANT: Carter, Paul J.  
PRESTA, Leonard G.  
TITLE OF INVENTION: Method for Making Humanized Antibodies  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/705,686  
FILING DATE: 02-NO. 6639055-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-705-686-18

Query Match 86.7%; Score 491; DB 4; Length 107;  
Best Local Similarity 91.6%; Pred. No. 2.8e-35;  
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCRAQGISNNLMHWYQOKPGKAPKLLIYHASQSIGVPS 60  
DB 1 DIQMTQSPSSLSASVGRVTITTCRAQGISNNLMHWYQOKPGKAPKLLIYHASQSIGVPS 60

QY 61 RFSSGSGTDFTLTISSLQPEDFATYYCOQNSWPTFGQGTKEIK 107  
DB 61 RFSSGSGTDFTLTISSLQPEDFATYYCOQNSLPTWFGQGTKEIK 107

RESULT 7  
PCT-US93-07832-18  
Sequence 18, Application PC/TUS9307832  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07832  
FILING DATE: 19930820  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 709P2PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE:  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US93-07832-18

Query Match 86.7%; Score 491; DB 5; Length 107;  
Best Local Similarity 91.6%; Pred. No. 2.8e-35;  
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVTTTCRASGSISSNNLHMVQOKPKAPKLLIYASGISGVPS 60  
DB 1 DIQWTQSPSSLSASVGRVTTTCRASGSISSNNLHMVQOKPKAPKLLIYASGISGVPS 60

QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMSPYFGGTKEIKR 107  
DB 61 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMSPYFGGTKEIKR 107

RESULT 8  
US-07-934-373C-3  
Sequence 3, Application US/07934373C  
Patent No. 5821337  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-07-934-373C-3

Query Match 86.7%; Score 491; DB 2; Length 109;  
Best Local Similarity 89.8%; Pred. No. 2.9e-35;  
Matches 97; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVTTTCRASGSISSNNLHMVQOKPKAPKLLIYASGISGVPS 60  
DB 1 DIQWTQSPSSLSASVGRVTTTCRASQDVSSYLAWYQOKPKAPKLLIYASGISGVPS 60

QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMSPYFGGTKEIKR 108  
DB 61 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMSPYFGGTKEIKR 108

RESULT 9  
US-08-437-642B-3  
Sequence 3, Application US/08437642B  
Patent No. 6054297  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/437,642B  
FILING DATE: 09-May-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994



TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-437-6428-3

Query Match 86.7%; Score 491; DB 3; Length 109;  
Best Local Similarity 89.8%; Pred. No. 2.9e-35;  
Matches 97; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSISASVGVGVITTCRASQISNNLMHYQKPKAKPLIYHASQISGVPS 60  
1 DIQWTGSPSSISASVGVGVITTCRASQISNNLMHYQKPKAKPLIYHASQISGVPS 60

QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCOQNSWPTYFGQGTKEIKR 108  
61 RFSGSGSGTDFTLTISLQPEDFATYYCOQNSWPTYFGQGTKEIKR 108

RESULT 10  
US-08-146-206C-3  
Sequence 3, Application US/08146206C  
Patent No. 6407213  
GENERAL INFORMATION:  
APPLICANT: Carter, Paul J.  
PRESTA, Leonard G.  
TITLE OF INVENTION: Method for Making Humanized Antibodies  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146, 206C  
FILING DATE: 17-NOV-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-146-206C-3

Query Match 86.7%; Score 491; DB 4; Length 109;  
Best Local Similarity 89.8%; Pred. No. 2.9e-35;  
Matches 97; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSISASVGVGVITTCRASQISNNLMHYQKPKAKPLIYHASQISGVPS 60  
1 DIQWTGSPSSISASVGVGVITTCRASQISNNLMHYQKPKAKPLIYHASQISGVPS 60

QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCOQNSWPTYFGQGTKEIKR 108  
61 RFSGSGSGTDFTLTISLQPEDFATYYCOQNSWPTYFGQGTKEIKR 108

Db 61 RFSGSGSGTDFTLTISLQPEDFATYYCOQNSWPTYFGQGTKEIKR 108

RESULT 11  
US-09-705-686-3  
Sequence 3, Application US/09705686  
Patent No. 6639055  
GENERAL INFORMATION:  
APPLICANT: Carter, Paul J.  
PRESTA, Leonard G.  
TITLE OF INVENTION: Method for Making Humanized Antibodies  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/705, 686  
FILING DATE: 02-NOV-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-705-686-3

Query Match 86.7%; Score 491; DB 4; Length 109;  
Best Local Similarity 89.8%; Pred. No. 2.9e-35;  
Matches 97; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSISASVGVGVITTCRASQISNNLMHYQKPKAKPLIYHASQISGVPS 60  
1 DIQWTGSPSSISASVGVGVITTCRASQISNNLMHYQKPKAKPLIYHASQISGVPS 60

QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCOQNSWPTYFGQGTKEIKR 108  
61 RFSGSGSGTDFTLTISLQPEDFATYYCOQNSWPTYFGQGTKEIKR 108

RESULT 12  
PCT-US93-07832-3  
Sequence 3, Application PC/TUS9307832  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California

COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07832  
FILING DATE: 19930820  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 709P2PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE:  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO. 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US93-07832-3

Query Match 86.7%; Score 491; DB 5; Length 109;  
Best Local Similarity 89.8%; Pred. No. 2.9e-35;  
Matches 97; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQSISSNNLHWYQOKPGKAPKLLIYHASQISGVPS 60  
DB 1 DIQMTQSPSSLSASVGRVTITCRASQSDVSSYLAHYQOKPGKAPKLLIYHASQISGVPS 60

QY 61 RFGSGSGTDFLTITISLQPEDPATYCCQNSWPTFGQGTVEIKR 108  
DB 61 RFGSGSGTDFLTITISLQPEDPATYCCQNSLPTFGQGTVEIKR 108

RESULT 13  
US-09-157-370-3  
Sequence 3, Application US/09157370A  
Patent No. 6262238  
GENERAL INFORMATION:  
APPLICANT: STEINBACHER, Stefan  
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES  
FILE REFERENCE: P8341-8072  
CURRENT APPLICATION NUMBER: US/09/157,370A  
EARLIER FILING DATE: 1998-09-21  
EARLIER APPLICATION NUMBER: 08/765,179  
EARLIER FILING DATE: 1997-01-14  
EARLIER APPLICATION NUMBER: PCT/EP95/02626  
EARLIER FILING DATE: 1995-07-06  
EARLIER APPLICATION NUMBER: DE/P44 25 115.7  
EARLIER FILING DATE: 1994-07-15  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 109  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-157-370-3

Query Match 86.4%; Score 489; DB 3; Length 109;  
Best Local Similarity 90.7%; Pred. No. 4.3e-35;  
Matches 96; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQSISSNNLHWYQOKPGKAPKLLIYHASQISGVPS 60  
DB 1 DIQMTQSPSSLSASVGRVTITCRASQSISSYLAHYQOKPGKAPKLLIYHASQISGVPS 60

QY 61 RFGSGSGTDFLTITISLQPEDPATYCCQNSWPTFGQGTVEIKR 108  
DB 61 RFGSGSGTDFLTITISLQPEDPATYCCQYSLPTFGQGTVEIKR 108

RESULT 14  
US-07-934-373C-17  
Sequence 17, Application US/07934373C  
Patent No. 5821337  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
ATTORNEY/AGENT INFORMATION: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO. 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-07-934-373C-17

Query Match 85.2%; Score 482; DB 2; Length 107;  
Best Local Similarity 86.9%; Pred. No. 1.7e-34;  
Matches 93; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQSISSNNLHWYQOKPGKAPKLLIYHASQISGVPS 60  
DB 1 DIQMTQSPSSLSASVGRVTITCRASQSDIRVNLHWYQOKPGKAPKLLIYTSRLSAGVPS 60

QY 61 RFGSGSGTDFLTITISLQPEDPATYCCQNSWPTFGQGTVEIKR 107  
DB 61 RFGSGSGTDFLTITISLQPEDPATYCCQNGTLPWTFGQGTVEIKR 107

RESULT 15  
US-08-437-642B-17

Sequence 17, Application US/08437642B  
Patent No. 6054297  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Minipalin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/437,642B  
FILING DATE: 09-May-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-Aug-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-Nov-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-Jun-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-Jun-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-437-642B-17

Query Match 85.2%; Score 482; DB 3; Length 107;  
Best Local Similarity 86.9%; Pred. No. 1.7e-34;  
Matches 93; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSISASVGRVITTCRASQISNNLHWYQOKPGKAPKLLIYHASQISGVPS 60  
|||  
DB 1 DIQWTQSPSSISASVGRVITTCRASQISNNLHWYQOKPGKAPKLLIYHASQISGVPS 60  
|||  
QY 61 RFGSGSGGTDTLTITSSIQPEDFATYYCQGSNWPYTFGGTKVEIK 107  
|||  
DB 61 RFGSGSGGTDTLTITSSIQPEDFATYYCQGSNWPYTFGGTKVEIK 107  
|||

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Job time : 48.2143 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 16:57:28 ; Search time 51.7857 Seconds  
(without alignments)  
115.642 Million cell updates/sec

Title: US-09-910-483-5  
Perfect score: 617  
Sequence: 1 EVGLVBSGGGLVQPGSLRL.....TASGYWFAWYGGTLYTVSS 116

Scoring table:  
BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/iaa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/2/iaa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/2/iaa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/2/iaa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/2/iaa/PTUTS.COMB.pep: \*  
6: /cgn2\_6/ptodata/2/iaa/backfilest.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	518	84.0	120	2	US-07-934-373C-42
2	518	84.0	120	3	US-08-437-642B-42
3	518	84.0	449	4	US-09-679-397-2
4	518	84.0	449	4	US-09-680-148-2
5	518	84.0	449	4	US-09-304-465A-2
6	518	84.0	461	2	US-08-463-587A-26
7	518	84.0	461	2	US-08-463-667A-4
8	518	84.0	461	2	US-08-923-854-26
9	518	84.0	461	5	PCT-US91-09133-27
10	510	82.7	120	2	US-07-934-373C-2
11	510	82.7	120	2	US-07-934-373C-48
12	510	82.7	120	3	US-08-437-642B-2
13	510	82.7	120	4	US-08-146-206C-2
14	510	82.7	120	4	US-09-705-686-2
15	510	82.7	120	5	PCT-US93-07832-2
16	504	81.7	120	2	US-07-934-373C-44
17	504	81.7	120	3	US-08-437-642B-44
18	471.5	76.4	119	1	US-08-053-171-12
19	468.5	75.9	467	1	US-08-704-744-81
20	462	74.9	122	2	US-07-934-373C-45
21	462	74.9	122	3	US-08-437-642B-45
22	462	74.9	122	4	US-08-146-206C-26
23	462	74.9	122	4	US-09-705-686-26
24	458	74.2	253	3	US-09-027-449-52
25	458	74.2	253	3	US-09-027-449-55
26	458	74.2	253	3	US-08-804-444A-52
27	458	74.2	253	3	US-08-804-444A-55

28	458	74.2	253	3	US-09-026-985-52	Sequence 52, Appl
29	458	74.2	253	3	US-09-026-985-55	Sequence 55, Appl
30	458	74.2	253	4	US-09-121-952A-52	Sequence 52, Appl
31	458	74.2	253	4	US-09-121-952A-55	Sequence 55, Appl
32	458	74.2	253	4	US-09-234-340A-52	Sequence 52, Appl
33	458	74.2	253	4	US-09-234-340A-55	Sequence 55, Appl
34	458	74.2	256	3	US-09-027-449-70	Sequence 70, Appl
35	458	74.2	256	3	US-09-026-985-70	Sequence 70, Appl
36	458	74.2	256	4	US-09-121-952A-70	Sequence 70, Appl
37	458	74.2	256	4	US-09-234-340A-70	Sequence 70, Appl
38	458	74.2	298	3	US-09-027-449-60	Sequence 60, Appl
39	458	74.2	298	3	US-08-804-444A-60	Sequence 60, Appl
40	458	74.2	298	3	US-09-026-985-60	Sequence 60, Appl
41	458	74.2	298	4	US-09-121-952A-60	Sequence 60, Appl
42	458	74.2	298	4	US-09-234-340A-60	Sequence 60, Appl
43	458	74.2	452	3	US-09-027-449-71	Sequence 71, Appl
44	458	74.2	452	3	US-09-026-985-71	Sequence 71, Appl
45	458	74.2	452	4	US-09-121-952A-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1  
US-07-934-373C-42  
Sequence 42, Application US/07934373C  
Patent No. 3821337  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-07-934-373C-42  
Query Match 84.0%; Score 518; DB 2; Length 120;  
Best Local Similarity 85.8%; Pred. No. 2.1e-42;  
Matches 103; Conservative 2; Mismatches 11; Gaps 1;  
QY 1 EVGLVBSGGGLVQPGSLRLSCASGNFKDTYIHWVRQAPGKGLIEWVARIDPANDNTIY 60

Db 1 EVOLVESGGGLVOPGSLRLSCAASGFMNKTQYIHVWRQAPGKLEWVARIPDNDNTIY 60  
QY 61 ADSVKGRFTISDSDSKNTAYLQWNSLRADTAIVYYCTASG----YMFAYWGQGLTVTVSS 116  
Db 61 ADSVKGRFTISDTSKNTAYLQWNSLRADTAIVYYCSRWDGDFYAMDYWGQGLTVTVSS 120

## RESULT 2

US-08-437-642B-42  
; Sequence 42, Application US/08437642B  
; Patent No. 6054297  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/437,642B  
; FILING DATE: 09-May-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/934373  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/146206  
; FILING DATE: 17-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-08-437-642B-42

Query Match 84.0%; Score 518; DB 3; Length 120;  
Best Local Similarity 85.8%; Pred. No. 2.1e-42;  
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFMNKTQYIHVWRQAPGKLEWVARIPDNDNTIY 60  
Db 1 EVOLVESGGGLVOPGSLRLSCAASGFMNKTQYIHVWRQAPGKLEWVARIPDNDNTIY 60  
QY 61 ADSVKGRFTISDSDSKNTAYLQWNSLRADTAIVYYCTASG----YMFAYWGQGLTVTVSS 116  
Db 61 ADSVKGRFTISDTSKNTAYLQWNSLRADTAIVYYCSRWDGDFYAMDYWGQGLTVTVSS 120

## RESULT 3

US-09-679-397-2  
; Sequence 2, Application US/09679397  
; Patent No. 6339142  
; GENERAL INFORMATION:  
; APPLICANT: BASEY, CAROL D.  
; APPLICANT: BLANK, GREG S.  
; TITLE OF INVENTION: PROTEIN PURIFICATION  
; FILE REFERENCE: P1241R1D2  
; CURRENT APPLICATION NUMBER: US/09/679,397  
; PRIOR APPLICATION NUMBER: US 60/084,459  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: US 09/304,465  
; PRIOR FILING DATE: 1999-05-03  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 2  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence is synthesized.  
; US-09-679-397-2

Query Match 84.0%; Score 518; DB 4; Length 449;  
Best Local Similarity 85.8%; Pred. No. 9.3e-42;  
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFMNKTQYIHVWRQAPGKLEWVARIPDNDNTIY 60  
Db 1 EVOLVESGGGLVOPGSLRLSCAASGFMNKTQYIHVWRQAPGKLEWVARIPDNDNTIY 60  
QY 61 ADSVKGRFTISDSDSKNTAYLQWNSLRADTAIVYYCTASG----YMFAYWGQGLTVTVSS 116  
Db 61 ADSVKGRFTISDTSKNTAYLQWNSLRADTAIVYYCSRWDGDFYAMDYWGQGLTVTVSS 120

RESULT 4  
US-09-680-148-2  
; Sequence 2, Application US/09680148  
; Patent No. 6417335  
; GENERAL INFORMATION:  
; APPLICANT: BASEY, CAROL D.  
; APPLICANT: BLANK, GREG S.  
; TITLE OF INVENTION: PROTEIN PURIFICATION  
; FILE REFERENCE: P1241R1D1  
; CURRENT APPLICATION NUMBER: US/09/680,148  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: US 60/084,459  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: US 09/304,465  
; PRIOR FILING DATE: 1999-05-03  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 2  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence is synthesized.  
; Patent No. 6417335  
; US-09-680-148-2

Query Match 84.0%; Score 518; DB 4; Length 449;  
Best Local Similarity 85.8%; Pred. No. 9.3e-42;  
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFMNKTQYIHVWRQAPGKLEWVARIPDNDNTIY 60  
Db 1 EVOLVESGGGLVOPGSLRLSCAASGFMNKTQYIHVWRQAPGKLEWVARIPDNDNTIY 60  
QY 61 ADSVKGRFTISDSDSKNTAYLQWNSLRADTAIVYYCTASG----YMFAYWGQGLTVTVSS 116  
Db 61 ADSVKGRFTISDTSKNTAYLQWNSLRADTAIVYYCSRWDGDFYAMDYWGQGLTVTVSS 120

```

RESULT 5
US-09-304-465A-2
; Sequence 2, Application US/09304465A
; Patent No. 6489447
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R1
; CURRENT APPLICATION NUMBER: US/09/304,465A
; CURRENT FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6489447
US-09-304-465A-2

Query Match      84.0%; Score 518; DB 4; Length 449;
Best Local Similarity 85.8%; Pred. No. 9.3e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY      1 EVQLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDTIY 60
DB      1 EVQLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIPPTNGTRY 60
        1 EVQLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIPPTNGTRY 60
        61 ADVYKGRFTISADTSKNTAYLQNNSLRAEDTAVYYCSRWDGDFYAMDYWGQGLTVTVSS 120
        61 ADVYKGRFTISDSDSKNTAYLQNNSLRAEDTAVYYCTASG---YWPAYWGQGLTVTVSS 116
        61 ADVYKGRFTISADTSKNTAYLQNNSLRAEDTAVYYCSRWDGDFYAMDYWGQGLTVTVSS 120

RESULT 6
US-08-463-587A-26
; Sequence 26, Application US/08463587A
; Patent No. 5821047
; GENERAL INFORMATION:
; APPLICANT: Garrard, Lisa J.
; APPLICANT: Henner, Dennis J.
; APPLICANT: Bass, Steven
; APPLICANT: Greene, Ronald
; APPLICANT: Lowman, Henry B.
; APPLICANT: Wells, James A.
; APPLICANT: Matthews, David J.
; TITLE OF INVENTION: ENRICHMENT METHOD FOR VARIANT PROTEINS WITH
; TITLE OF INVENTION: ALTERED BINDING PROPERTIES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,587A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/050058
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09133

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; FILING DATE: 03-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743614
; FILING DATE: 09-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715300
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/683400
; FILING DATE: 10-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/621667
; FILING DATE: 03-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P0645P4D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/952-9867
; TELEFAX: 415/952-9861
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-463-587A-26

Query Match      84.0%; Score 518; DB 2; Length 461;
Best Local Similarity 85.8%; Pred. No. 9.6e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY      1 EVQLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDTIY 60
DB      24 EVQLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIPPTNGTRY 83
        24 EVQLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIPPTNGTRY 83
        61 ADVYKGRFTISDSDSKNTAYLQNNSLRAEDTAVYYCTASG---YWPAYWGQGLTVTVSS 116
        84 ADVYKGRFTISADTSKNTAYLQNNSLRAEDTAVYYCSRWDGDFYAMDYWGQGLTVTVSS 143

RESULT 7
US-08-463-667A-4
; Sequence 4, Application US/08463667A
; Patent No. 5834598
; GENERAL INFORMATION:
; APPLICANT: Garrard, Lisa J.
; APPLICANT: Henner, Dennis J.
; APPLICANT: Bass, Steven
; APPLICANT: Greene, Ronald
; APPLICANT: Lowman, Henry B.
; APPLICANT: Wells, James A.
; APPLICANT: Matthews, David J.
; TITLE OF INVENTION: ENRICHMENT METHOD FOR VARIANT PROTEINS
; TITLE OF INVENTION: WITH ALTERED BINDING PROPERTIES
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,667A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: US 08/050,058
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US91/09133
; FILING DATE: 03-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,614
; FILING DATE: 09-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/715,300
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/683,400
; FILING DATE: 10-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,667
; FILING DATE: 03-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Daryl B.
; REGISTRATION NUMBER: 32,637
; REFERENCE/DOCKET NUMBER: 645PAD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 225-1249
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-463-667A-4

Query Match      84.0%; Score 518; DB 2; Length 461;
Best Local Similarity 85.8%; Pred. No. 9.6e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVLVESGGGLVOPGSGSLRSLSCAASGFNIKDTYIHWVROAPGKLEWVARIDPANDNTIY 60
DB 24 EVLVESGGGLVOPGSGSLRSLSCAASGFNIKDTYIHWVROAPGKLEWVARIPTNGYTRY 83
QY 61 ADSVKGRFTISSDSKNTAYLQNNSLRAEDTAVYYCTASG---YFAYWGQGLTVTVSS 116
DB 84 ADSVKGRFTISADTISKNTAYLQNNSLRAEDTAVYYCSRWGSDGFYAMDYWGQGLTVTVSS 143

RESULT 8
US-08-923-854-26
; Sequence 26, Application US/08923854
; Patent No. 6040136
; GENERAL INFORMATION:
; APPLICANT: Garrard, Lisa J.
; APPLICANT: Henner, Dennis J.
; APPLICANT: Bass, Steven
; APPLICANT: Greene, Ronald
; APPLICANT: Lowman, Henry B.
; APPLICANT: Matthews, David J.
; TITLE OF INVENTION: ENRICHMENT METHOD FOR VARIANT PROTEINS WITH
; TITLE OF INVENTION: ALTERED BINDING PROPERTIES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/463587
; FILING DATE: 05-Jun-1995
; APPLICATION NUMBER: 08/050058
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09133
; FILING DATE: 03-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743614
; FILING DATE: 09-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715300
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/683400
; FILING DATE: 10-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/621667
; FILING DATE: 03-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P0645PAD2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-7467
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: Amino Acid
; TOPOLOGY: linear
; US-08-923-854-26

Query Match      84.0%; Score 518; DB 3; Length 461;
Best Local Similarity 85.8%; Pred. No. 9.6e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVLVESGGGLVOPGSGSLRSLSCAASGFNIKDTYIHWVROAPGKLEWVARIDPANDNTIY 60
DB 24 EVLVESGGGLVOPGSGSLRSLSCAASGFNIKDTYIHWVROAPGKLEWVARIPTNGYTRY 83
QY 61 ADSVKGRFTISSDSKNTAYLQNNSLRAEDTAVYYCTASG---YFAYWGQGLTVTVSS 116
DB 84 ADSVKGRFTISADTISKNTAYLQNNSLRAEDTAVYYCSRWGSDGFYAMDYWGQGLTVTVSS 143

RESULT 9
PCT-US91-09133-27
; Sequence 27, Application PC/TUS9109133
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Garrard, Lisa J.
; APPLICANT: Henner, Dennis J.
; APPLICANT: Bass, Steven
; APPLICANT: Greene, Ronald
; APPLICANT: Lowman, Henry B.
; APPLICANT: Matthews, David J.
; TITLE OF INVENTION: Enrichment Method For Variant Proteins
; TITLE OF INVENTION: With Altered Binding Properties
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
```



ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/09133  
FILING DATE: 19911203  
CLASSIFICATION: 425  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/743614  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715300  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/683400  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/621667  
ATTORNEY/AGENT INFORMATION:  
NAME: Benson, Robert H.  
REGISTRATION NUMBER: 30,446  
REFERENCE/DOCKET INFORMATION: 645P4  
TELEPHONE: 415/266-1489  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 461 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
PCT-US91-09133-27

Query Match 84.0%; Score 518; DB 5; Length 461;  
Best Local Similarity 85.8%; Pred. No. 9.6e-42;  
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGPNIKDTYIHWVROAPGKLEWVARIDPANDNTIY 60  
DB 24 EVOLVESGGGLVOPGSLRLSCAASGPNIKDTYIHWVROAPGKLEWVARIDPANDNTIY 83  
QY 61 ADVYKGRFTISSDSKNTAYLQWNSLRAPDPAVYYCTASG---YMFAYMGQGLTVYSS 116  
DB 84 ADVYKGRFTISADTSKNTAYLQWNSLRAPDPAVYYCSRWDGDFYANDVWGQGLTVYSS 143

RESULT 10  
US-07-934-373C-2  
Sequence 2, Application US/07934373C  
Patent No. 5821337  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126

FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-07-934-373C-2

Query Match 82.7%; Score 510; DB 2; Length 120;  
Best Local Similarity 85.0%; Pred. No. 1.2e-41;  
Matches 102; Conservative 2; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGPNIKDTYIHWVROAPGKLEWVARIDPANDNTIY 60  
DB 1 EVOLVESGGGLVOPGSLRLSCAASGPNIKDTYIHWVROAPGKLEWVARIDPANDNTIY 60  
QY 61 ADVYKGRFTISSDSKNTAYLQWNSLRAPDPAVYYCTASG---YMFAYMGQGLTVYSS 116  
DB 61 ADVYKGRFTISADTSKNTAYLQWNSLRAPDPAVYYCSRWDGDFYANDVWGQGLTVYSS 120

RESULT 11  
US-07-934-373C-48  
Sequence 48, Application US/07934373C  
Patent No. 5821337  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid

TOPOLOGY: Linear  
US-07-934-373C-48

Query Match 82.7%; Score 510; DB 2; Length 120;  
Best Local Similarity 85.0%; Pred. No. 1.2e-41;  
Matches 102; Conservative 2; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIPDNDNTY 60  
DB 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIPDNTY 60  
QY 61 ADSVKGRFTISDPSKNTAYLQNMNLSRAEDTAVYYCTASG---YWFAYWGQGLTVTVSS 116  
DB 61 ADSVKGRFTISADTSKNTAYLQNMNLSRAEDTAVYYCSRWGSDGFYAMDVMGQGLTVTVSS 120

RESULT 12  
US-08-437-642B-2

; Sequence 2, Application US/08437642B  
; Patent No. 6054297  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/437,642B  
; FILING DATE: 09-May-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/934373  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/146206  
; FILING DATE: 17-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-08-437-642B-2

Query Match 82.7%; Score 510; DB 3; Length 120;

Best Local Similarity 85.0%; Pred. No. 1.2e-41;  
Matches 102; Conservative 2; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIPDNDNTY 60  
DB 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIPDNDNTY 60

DB 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIPDNTY 60

QY 61 ADSVKGRFTISDPSKNTAYLQNMNLSRAEDTAVYYCTASG---YWFAYWGQGLTVTVSS 116  
DB 61 ADSVKGRFTISADTSKNTAYLQNMNLSRAEDTAVYYCSRWGSDGFYAMDVMGQGLTVTVSS 120

RESULT 13  
US-08-146-206C-2

; Sequence 2, Application US/08146206C  
; Patent No. 6407213  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Method for Making Humanized Antibodies  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/146,206C  
; FILING DATE: 17-No. 6407213-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-08-146-206C-2

Query Match 82.7%; Score 510; DB 4; Length 120;  
Best Local Similarity 85.0%; Pred. No. 1.2e-41;  
Matches 102; Conservative 2; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIPDNDNTY 60  
DB 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIPDNTY 60  
QY 61 ADSVKGRFTISDPSKNTAYLQNMNLSRAEDTAVYYCTASG---YWFAYWGQGLTVTVSS 116  
DB 61 ADSVKGRFTISADTSKNTAYLQNMNLSRAEDTAVYYCSRWGSDGFYAMDVMGQGLTVTVSS 120

RESULT 14

US-09-705-686-2

; Sequence 2, Application US/09705686  
; Patent No. 6639055  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Method for Making Humanized Antibodies  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.

```

STREET: 1 DNA Way
City: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-NO. 6639055-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-705-686-2

```

```

Query Match      82.7%; Score 510; DB 4; Length 120;
Best Local Similarity 85.0%; Pred. No. 1.2e-41;
Matches 102; Conservative 2; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSGSLRLSCAASGFINIKDTYIHWYRQAPGKGLVWVARIDPANDNTIY 60
Db 1 EVOLVESGGGLVOPGSGSLRLSCAASGFINIKDTYIHWYRQAPGKGLVWVARIYPTNGYTRY 60

QY 61 ADSVKGKFTTSSDPSKNTAYLQNMNLSRAEDTAVYYCTASG----YMFAYWGQGLTVTVSS 116
Db 61 ADSVKGKFTTSSDPSKNTAYLQNMNLSRAEDTAVYYCTASG----YMFAYWGQGLTVTVSS 120

```

```

RESULT 15
PCT-US93-07832-2
Sequence 2, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991

```

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX: 415/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: Linear
PCT-US93-07832-2

```

```

Query Match      82.7%; Score 510; DB 5; Length 120;
Best Local Similarity 85.0%; Pred. No. 1.2e-41;
Matches 102; Conservative 2; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVOPGSGSLRLSCAASGFINIKDTYIHWYRQAPGKGLVWVARIDPANDNTIY 60
Db 1 EVOLVESGGGLVOPGSGSLRLSCAASGFINIKDTYIHWYRQAPGKGLVWVARIYPTNGYTRY 60

QY 61 ADSVKGKFTTSSDPSKNTAYLQNMNLSRAEDTAVYYCTASG----YMFAYWGQGLTVTVSS 116
Db 61 ADSVKGKFTTSSDPSKNTAYLQNMNLSRAEDTAVYYCTASG----YMFAYWGQGLTVTVSS 120

```

Search completed: May 13, 2004, 17:05:04  
Job time : 51.7857 secs

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```
Sequence 7, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain
US-09-910-483-7
```

```
Query Match          100.0%; Score 566; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.2e-40;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQSPSSLSASVDGRVTITCRASQISNNLHWYQKPKGLIYHASQSIGVPS 60
DB 1 DIQMTQSPSSLSASVDGRVTITCRASQISNNLHWYQKPKGLIYHASQSIGVPS 60
QY 61 RFSGSGSGTDFTLTISLSLOPEDPATYTCQOSNSWPTFGQGTKEIKR 108
DB 61 RFSGSGSGTDFTLTISLSLOPEDPATYTCQOSNSWPTFGQGTKEIKR 108
```

## RESULT 3

```
US-09-910-483-11
; Sequence 11, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain
US-09-910-483-11
```

```
Query Match          100.0%; Score 566; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.2e-40;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQSPSSLSASVDGRVTITCRASQISNNLHWYQKPKGLIYHASQSIGVPS 60
DB 1 DIQMTQSPSSLSASVDGRVTITCRASQISNNLHWYQKPKGLIYHASQSIGVPS 60
QY 61 RFSGSGSGTDFTLTISLSLOPEDPATYTCQOSNSWPTFGQGTKEIKR 108
DB 61 RFSGSGSGTDFTLTISLSLOPEDPATYTCQOSNSWPTFGQGTKEIKR 108
```

```
RESULT 4
US-09-910-483-15
; Sequence 15, Application US/09910483
```

```
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain
US-09-910-483-15
```

```
Query Match          100.0%; Score 566; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.2e-40;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQSPSSLSASVDGRVTITCRASQISNNLHWYQKPKGLIYHASQSIGVPS 60
DB 1 DIQMTQSPSSLSASVDGRVTITCRASQISNNLHWYQKPKGLIYHASQSIGVPS 60
QY 61 RFSGSGSGTDFTLTISLSLOPEDPATYTCQOSNSWPTFGQGTKEIKR 108
DB 61 RFSGSGSGTDFTLTISLSLOPEDPATYTCQOSNSWPTFGQGTKEIKR 108
```

## RESULT 5

```
US-09-910-483-19
; Sequence 19, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain
US-09-910-483-19
```

```
Query Match          100.0%; Score 566; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.2e-40;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQSPSSLSASVDGRVTITCRASQISNNLHWYQKPKGLIYHASQSIGVPS 60
DB 1 DIQMTQSPSSLSASVDGRVTITCRASQISNNLHWYQKPKGLIYHASQSIGVPS 60
QY 61 RFSGSGSGTDFTLTISLSLOPEDPATYTCQOSNSWPTFGQGTKEIKR 108
DB 61 RFSGSGSGTDFTLTISLSLOPEDPATYTCQOSNSWPTFGQGTKEIKR 108
```

```
RESULT 6
US-09-910-483-23
; Sequence 23, Application US/09910483
; Publication No. US20030035798A1
```

```

; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain
; OTHER INFORMATION: peptide of Hum F
US-09-910-483-23
```

```

Query Match          100.0%; Score 566; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.2e-40;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 DIQWTSPPSSLSASVGDRTVITTCRASQISNNLHMWYQOKPKAPKLIYHASQISGVPS 60
DB 1 DIQWTSPPSSLSASVGDRTVITTCRASQISNNLHMWYQOKPKAPKLIYHASQISGVPS 60
```

```

QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCOQSNMWPYTFGGCTKVEIKR 108
DB 61 RFSGSGSGTDFTLTISLQPEDFATYYCOQSNMWPYTFGGCTKVEIKR 108
```

```

RESULT 7
US-09-910-483-44
```

```

; Sequence 44, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 44
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanized I16
; OTHER INFORMATION: (HumI9) VH domain consensus sequence of light chain K
; OTHER INFORMATION: Subgroup I (HumKI)
US-09-910-483-44
```

```

Query Match          100.0%; Score 566; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.2e-40;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 DIQWTSPPSSLSASVGDRTVITTCRASQISNNLHMWYQOKPKAPKLIYHASQISGVPS 60
DB 1 DIQWTSPPSSLSASVGDRTVITTCRASQISNNLHMWYQOKPKAPKLIYHASQISGVPS 60
```

```

QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCOQSNMWPYTFGGCTKVEIKR 108
DB 61 RFSGSGSGTDFTLTISLQPEDFATYYCOQSNMWPYTFGGCTKVEIKR 108
```

```

RESULT 8
US-09-910-483-27
; Sequence 27, Application US/09910483
; Publication No. US20030035798A1
```

```

; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain
; OTHER INFORMATION: peptide of Hum G
US-09-910-483-27
```

```

Query Match          98.4%; Score 557; DB 10; Length 108;
Best Local Similarity 99.1%; Pred. No. 1.3e-39;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 DIQWTSPPSSLSASVGDRTVITTCRASQISNNLHMWYQOKPKAPKLIYHASQISGVPS 60
DB 1 DIQWTSPPSSLSASVGDRTVITTCRASQISNNLHMWYQOKPKAPKLIYHASQISGVPS 60
```

```

QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCOQSNMWPYTFGGCTKVEIKR 108
DB 61 RFSGSGSGTDFTLTISLQPEDFATYYCOQSNMWPYTFGGCTKVEIKR 108
```

```

RESULT 9
US-09-910-483-31
```

```

; Sequence 31, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTADT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain
; OTHER INFORMATION: peptide of Hum H
US-09-910-483-31
```

```

Query Match          98.4%; Score 557; DB 10; Length 108;
Best Local Similarity 99.1%; Pred. No. 1.3e-39;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 DIQWTSPPSSLSASVGDRTVITTCRASQISNNLHMWYQOKPKAPKLIYHASQISGVPS 60
DB 1 DIQWTSPPSSLSASVGDRTVITTCRASQISNNLHMWYQOKPKAPKLIYHASQISGVPS 60
```

```

QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCOQSNMWPYTFGGCTKVEIKR 108
DB 61 RFSGSGSGTDFTLTISLQPEDFATYYCOQSNMWPYTFGGCTKVEIKR 108
```

```

RESULT 10
US-09-910-483-35
; Sequence 35, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
```

APPLICANT: FANG, FANG  
APPLICANT: KOHLSTADT, LORI  
APPLICANT: RENO, JOHN  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
FILE REFERENCE: 014357/027 8772  
CURRENT APPLICATION NUMBER: US/09/910,483  
CURRENT FILING DATE: 2001-07-19  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 35  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL Domain  
US-09-910-483-35

Query Match 98.4%; Score 557; DB 10; Length 108;  
Best Local Similarity 99.1%; Pred. No. 1,3e-39;  
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGRVITTCRASOSISNNLHWYQOKRGAAPKLLIYHASOSISGVPS 60  
DB 1 DIOMTOSPSLSASVGRVITTCRASOSISNNLHWYQOKRGAAPKLLIYHASOSISGVPS 60  
QY 61 RFGSGSGTDFTLTITSLQPEDFATYYCOQSNMWPYTFGQGTKEIR 108  
DB 61 RFGSGSGTDFTLTITSLQPEDFATYYCOQSNMWPYTFGQGTKEIR 108

RESULT 11  
US-10-223-880-17  
Sequence 17, Application US/10223880  
Publication No. US20030152571A1  
GENERAL INFORMATION:  
APPLICANT: JONAK, ZDENKA  
APPLICANT: JOHANSON, KYUNG O.  
APPLICANT: TAYLOR, ALEXANDER  
TITLE OF INVENTION: ANTI-ALPHA BETA 3 HUMANIZED MONOCLONAL  
FILE REFERENCE: P50629C1  
CURRENT APPLICATION NUMBER: US/10/223,880  
CURRENT FILING DATE: 2002-08-20  
PRIOR APPLICATION NUMBER: 09/380,910  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: PCT/US98/04987  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/039,609  
PRIOR FILING DATE: 1997-03-12  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17  
LENGTH: 105  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Wherein the sequences represent the DNA and amino  
OTHER INFORMATION: acid sequences of the Jk gene and its gene  
OTHER INFORMATION: product.  
US-10-223-880-17

Query Match 89.0%; Score 504; DB 14; Length 105;  
Best Local Similarity 90.5%; Pred. No. 3.5e-35;  
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGRVITTCRASOSISNNLHWYQOKRGAAPKLLIYHASOSISGVPS 60  
DB 1 DIOMTOSPSLSASVGRVITTCRASOSISNNLHWYQOKRGAAPKLLIYHASOSISGVPS 60  
QY 61 RFGSGSGTDFTLTITSLQPEDFATYYCOQSNMWPYTFGQGTKEIR 105  
DB 61 RFGSGSGTDFTLTITSLQPEDFATYYCOQSNMWPYTFGQGTKEIR 105

RESULT 12  
US-10-223-880-21

Sequence 21, Application US/10223880  
Publication No. US20030152571A1  
GENERAL INFORMATION:  
APPLICANT: JONAK, ZDENKA  
APPLICANT: JOHANSON, KYUNG O.  
APPLICANT: TAYLOR, ALEXANDER  
TITLE OF INVENTION: ANTI-ALPHA BETA 3 HUMANIZED MONOCLONAL  
FILE REFERENCE: P50629C1  
CURRENT APPLICATION NUMBER: US/10/223,880  
CURRENT FILING DATE: 2002-08-20  
PRIOR APPLICATION NUMBER: 09/380,910  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: PCT/US98/04987  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/039,609  
PRIOR FILING DATE: 1997-03-12  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 21  
LENGTH: 105  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Represents an amino acid sequence of the synthetic  
OTHER INFORMATION: kappa chain based on a modified human Rk1 kappa  
OTHER INFORMATION: chain framework  
US-10-223-880-21

Query Match 89.0%; Score 504; DB 14; Length 105;  
Best Local Similarity 90.5%; Pred. No. 3.5e-35;  
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGRVITTCRASOSISNNLHWYQOKRGAAPKLLIYHASOSISGVPS 60  
DB 1 DIOMTOSPSLSASVGRVITTCRASOSISNNLHWYQOKRGAAPKLLIYHASOSISGVPS 60  
QY 61 RFGSGSGTDFTLTITSLQPEDFATYYCOQSNMWPYTFGQGTKEIR 105  
DB 61 RFGSGSGTDFTLTITSLQPEDFATYYCOQSNMWPYTFGQGTKEIR 105

RESULT 13  
US-09-056-160B-12

Sequence 12, Application US/09056160B  
Patent No. US20020032315A1  
GENERAL INFORMATION:  
APPLICANT: Baca, Manuel  
APPLICANT: Wells, James A.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Lowman, Henry B.  
APPLICANT: Chen, Yvonne M.  
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
NUMBER OF SEQUENCES: 131  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,160B  
FILING DATE: 06-Apr-1998



CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/054,856  
FILING DATE: 06-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Haack, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1093R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear

US-09-056-160B-12  
Query Match 87.6%; Score 496; DB 9; Length 108;  
Best Local Similarity 91.7%; Pred. No. 1,7e-34;  
Matches 99; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRTVITTCRASQSISSNNLHMVYQKPKKLIYASQISGVPS 60  
DB 1 DIQWTGSPSSLSASVGDRTVITTCRASQSISSNNLHMVYQKPKKLIYASQISGVPS 60  
QY 61 RFGSGSGGTDFTLTISLQPEDPATYCCQNSNMPYFGGTKEIKR 108  
DB 61 RFGSGSGGTDFTLTISLQPEDPATYCCQNSNMPYFGGTKEIKR 108

## RESULT 14

US-09-795-798-3  
Sequence 3, Application US/09795798  
Publication No. US20030207336A1  
GENERAL INFORMATION:  
APPLICANT: Presta, Leonard G.  
Jardieu, Paula M.  
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/795,798  
FILING DATE: 28-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/974,899  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P1014R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-795-798-3

Query Match 87.6%; Score 496; DB 11; Length 108;  
Best Local Similarity 91.7%; Pred. No. 1,7e-34;  
Matches 99; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRTVITTCRASQSISSNNLHMVYQKPKKLIYASQISGVPS 60  
DB 1 DIQWTGSPSSLSASVGDRTVITTCRASQSISSNNLHMVYQKPKKLIYASQISGVPS 60  
QY 61 RFGSGSGGTDFTLTISLQPEDPATYCCQNSNMPYFGGTKEIKR 108  
DB 61 RFGSGSGGTDFTLTISLQPEDPATYCCQNSNMPYFGGTKEIKR 108

## RESULT 15

US-10-234-671-12  
Sequence 12, Application US/10234671  
Publication No. US20030190317A1  
GENERAL INFORMATION:

APPLICANT: Baca, Manuel  
Wells, James A.  
Presta, Leonard G.  
Lowman, Henry B.  
Chen, Yvonne M.  
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
NUMBER OF SEQUENCES: 131  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/234,671  
FILING DATE: 03-Sep-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/056160  
FILING DATE: 06-APR-1998  
APPLICATION NUMBER: 60/126446  
FILING DATE: 07-APR-1997  
APPLICATION NUMBER: 60/054856  
FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Cui, Steven X.  
REGISTRATION NUMBER: 44,637  
REFERENCE/DOCKET NUMBER: P1093R2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-10-234-671-12

Query Match 87.6%; Score 496; DB 14; Length 108;  
Best Local Similarity 91.7%; Pred. No. 1,7e-34;  
Matches 99; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRTVITTCRASQSISSNNLHMVYQKPKKLIYASQISGVPS 60  
DB 1 DIQWTGSPSSLSASVGDRTVITTCRASQSISSNNLHMVYQKPKKLIYASQISGVPS 60  
QY 61 RFGSGSGGTDFTLTISLQPEDPATYCCQNSNMPYFGGTKEIKR 108

Fri May 14 07:50:48 2004

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Page 6

Db 61 RFGSGSGSTDFTLTITISLQPEDFATYCCQYNSLPLWTFQGTKEIKR 108

Search completed: May 13, 2004, 17:34:31  
Job time : 172.143 secs

GenCore version 5.1.6  
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OM:protein - protein search, using sw model

Run on: May 13, 2004, 17:03:18 ; Search time 184.357 Seconds  
(without alignments)  
175.086 Million cell updates/sec

Title: US-09-910-483-5

Perfect score: 617  
Sequence: 1 EVOLVESGGGLVQPGSLRL.....TASGYWFAWMGQGLTVYSS 116

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

- 1: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep.\*
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- 5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubppaa/PCTUS\_PUBCOMB.pep.\*
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- 9: /cgn2\_6/ptodata/2/pubppaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubppaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubppaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubppaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	617	100.0	116	10	US-09-910-483-5
2	617	100.0	116	10	US-09-910-483-43
3	613	99.4	116	10	US-09-910-483-13
4	611	98.9	116	10	US-09-910-483-1
5	610	98.9	116	10	US-09-910-483-21
6	610	98.9	116	10	US-09-910-483-25
7	609	98.7	116	10	US-09-910-483-9
8	589	95.5	116	10	US-09-910-483-17
9	589	95.5	116	10	US-09-910-483-29
10	576	93.4	116	10	US-09-910-483-33
11	518	84.0	120	9	US-09-971-543-11
12	518	84.0	120	12	US-10-411-037-36
13	518	84.0	120	12	US-10-411-026-36
14	518	84.0	120	15	US-10-410-894-2
15	518	84.0	120	16	US-10-410-962-36

16	518	84.0	120	16	US-10-411-049-36	Sequence 36, Appl
17	518	84.0	228	12	US-10-364-953-14	Sequence 14, Appl
18	518	84.0	252	9	US-09-971-543-1	Sequence 1, Appl
19	518	84.0	449	14	US-10-253-366-2	Sequence 2, Appl
20	518	84.0	449	14	US-10-316-694-2	Sequence 2, Appl
21	518	84.0	449	14	US-10-356-974-2	Sequence 2, Appl
22	518	84.0	449	15	US-10-423-299-2	Sequence 2, Appl
23	518	84.0	449	16	US-10-659-825-2	Sequence 2, Appl
24	518	84.0	527	12	US-10-182-975-25	Sequence 25, Appl
25	518	84.0	763	15	US-10-418-836-13	Sequence 13, Appl
26	518	84.0	979	15	US-10-418-836-16	Sequence 10, Appl
27	518	84.0	979	15	US-10-418-836-16	Sequence 16, Appl
28	480	77.8	116	10	US-09-910-483-37	Sequence 37, Appl
29	480	77.8	116	10	US-09-910-483-41	Sequence 41, Appl
30	471.5	76.4	117	10	US-09-802-083-2	Sequence 2, Appl
31	471.5	76.4	117	14	US-10-165-732A-2	Sequence 2, Appl
32	471.5	76.4	117	14	US-10-172-785-2	Sequence 2, Appl
33	471.5	76.4	225	12	US-10-364-953-12	Sequence 12, Appl
34	471.5	76.4	470	14	US-10-020-786-9	Sequence 9, Appl
35	471.5	76.4	470	14	US-10-327-694-5	Sequence 5, Appl
36	464.5	75.3	291	12	US-10-406-830-1	Sequence 1, Appl
37	464.5	75.3	291	12	US-10-406-830-2	Sequence 2, Appl
38	459.5	74.5	248	10	US-09-880-748-1421	Sequence 1421, Ap
39	459.5	74.5	248	12	US-10-293-418-1421	Sequence 1421, Ap
40	458.5	74.3	119	14	US-10-073-644C-2	Sequence 2, Appl
41	458	74.2	253	10	US-09-726-258-52	Sequence 52, Appl
42	458	74.2	253	10	US-09-726-258-55	Sequence 55, Appl
43	458	74.2	256	10	US-09-726-258-70	Sequence 70, Appl
44	458	74.2	298	10	US-09-726-258-60	Sequence 60, Appl
45	458	74.2	452	10	US-09-726-258-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1  
US-09-910-483-5  
; Sequence 5, Application US/09910483  
; Publication No. US20030035798A1  
; GENERAL INFORMATION:  
; APPLICANT: FANG, FANG  
; APPLICANT: KOHLSTADT, LORI  
; APPLICANT: RENO, JOHN  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; FILE REFERENCE: 014357/027 8772  
; CURRENT FILING DATE: US/09/910.483  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VH Domain  
US-09-910-483-5

Query Match 100.0%; Score 617; DB 10; Length 116;  
Best Local Similarity 100.0%; Pred. No. 4.9e-52;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EVOLVESGGGLVQPGSLRLSCAASGNIKDTYHWVRQAPGKLEWVARIDPANDNTY 60  
DB 1 EVOLVESGGGLVQPGSLRLSCAASGNIKDTYHWVRQAPGKLEWVARIDPANDNTY 60  
QY 61 ADSYKGRFTTSDSKNTAYLQMNLSLAEDTAVYYCTASGYWFAWMGQGLTVYSS 116  
DB 61 ADSYKGRFTTSDSKNTAYLQMNLSLAEDTAVYYCTASGYWFAWMGQGLTVYSS 116  
RESULT 2  
US-09-910-483-43

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Sequence 43, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTAEDT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanized 1A6
; OTHER INFORMATION: (Hum19) VH Domain consensus sequence of Heavy Chain
; OTHER INFORMATION: Subgroup III (Hum111)
US-09-910-483-43
```

```
Query Match          100.0%; Score 617; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.9e-52;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGPNIKDTYIHWRQAPGKGLEWVARIDPANDNTIY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGPNIKDTYIHWRQAPGKGLEWVARIDPANDNTIY 60
QY 61 ADSVKGRFTISSDSSKNTAVYLQMSLRAEDTAVYYCTASGYFAYWGQGLTVTVSS 116
DB 61 ADSVKGRFTISSDSSKNTAVYLQMSLRAEDTAVYYCTASGYFAYWGQGLTVTVSS 116
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```
RESULT 3
US-09-910-483-13
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; Sequence 13, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTAEDT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VH Domain
; OTHER INFORMATION: peptide of Hum D
US-09-910-483-13
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```
Query Match          99.4%; Score 613; DB 10; Length 116;
Best Local Similarity 99.1%; Pred. No. 1.2e-51;
Matches 115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGPNIKDTYIHWRQAPGKGLEWVARIDPANDNTIY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGPNIKDTYIHWRQAPGKGLEWVARIDPANDNTIY 60
QY 61 ADSVKGRFTISSDSSKNTAVYLQMSLRAEDTAVYYCTASGYFAYWGQGLTVTVSS 116
DB 61 ADSVKGRFTISSDSSKNTAVYLQMSLRAEDTAVYYCTASGYFAYWGQGLTVTVSS 116
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```
RESULT 4
US-09-910-483-1
```

```
Sequence 1, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTAEDT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VH Domain
; OTHER INFORMATION: peptide of Hum A
US-09-910-483-1
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```
Query Match          99.0%; Score 611; DB 10; Length 116;
Best Local Similarity 99.1%; Pred. No. 1.9e-51;
Matches 115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGPNIKDTYIHWRQAPGKGLEWVARIDPANDNTIY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGPNIKDTYIHWRQAPGKGLEWVARIDPANDNTIY 60
QY 61 ADSVKGRFTISSDSSKNTAVYLQMSLRAEDTAVYYCTASGYFAYWGQGLTVTVSS 116
DB 61 ADSVKGRFTISSDSSKNTAVYLQMSLRAEDTAVYYCTASGYFAYWGQGLTVTVSS 116
```

```
RESULT 5
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```
US-09-910-483-21
; Sequence 21, Application US/09910483
; Publication No. US20030035798A1
; GENERAL INFORMATION:
; APPLICANT: FANG, FANG
; APPLICANT: KOHLSTAEDT, LORI
; APPLICANT: RENO, JOHN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; FILE REFERENCE: 014357/027 8772
; CURRENT APPLICATION NUMBER: US/09/910,483
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VH Domain
; OTHER INFORMATION: peptide of Hum F
US-09-910-483-21
```

```
Query Match          98.9%; Score 610; DB 10; Length 116;
Best Local Similarity 98.3%; Pred. No. 2.3e-51;
Matches 114; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGPNIKDTYIHWRQAPGKGLEWVARIDPANDNTIY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGPNIKDTYIHWRQAPGKGLEWVARIDPANDNTIY 60
QY 61 ADSVKGRFTISSDSSKNTAVYLQMSLRAEDTAVYYCTASGYFAYWGQGLTVTVSS 116
DB 61 ADSVKGRFTISSDSSKNTAVYLQMSLRAEDTAVYYCTASGYFAYWGQGLTVTVSS 116
```

```
RESULT 6
US-09-910-483-25
; Sequence 25, Application US/09910483
```

Publication No. US20030035798A1  
; GENERAL INFORMATION:  
; APPLICANT: FANG, FANG  
; APPLICANT: KOHLSTADT, LORI  
; APPLICANT: RENO, JOHN  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; FILE REFERENCE: 014357/027 8772  
; CURRENT APPLICATION NUMBER: US/09/910,483  
; CURRENT FILING DATE: 2001-07-19  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VH Domain  
; OTHER INFORMATION: peptide of Hum G  
US-09-910-483-25

Query Match 98.9%; Score 610; DB 10; Length 116;  
Best Local Similarity 98.3%; Pred. No. 2.3e-51;  
Matches 114; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTYY 60  
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTYY 60  
QY 61 ADVYKGRFTISSDDSKNTAYLQNMNSLRADPTAVYYCTASGYWFAWVGGLVTYSS 116  
DB 61 ADVYKGRFTISADDSKNTAYLQNMNSLRADPTAVYYCTTSGYWFAYWVGGLVTYSS 116

## RESULT 7

US-09-910-483-9  
; Sequence 9, Application US/09910483  
; Publication No. US20030035798A1  
; GENERAL INFORMATION:  
; APPLICANT: FANG, FANG  
; APPLICANT: KOHLSTADT, LORI  
; APPLICANT: RENO, JOHN  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; FILE REFERENCE: 014357/027 8772  
; CURRENT APPLICATION NUMBER: US/09/910,483  
; CURRENT FILING DATE: 2001-07-19  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VH Domain  
; OTHER INFORMATION: peptide of Hum C  
US-09-910-483-9

Query Match 98.7%; Score 609; DB 10; Length 116;  
Best Local Similarity 98.3%; Pred. No. 2.9e-51;  
Matches 114; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTYY 60  
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTYY 60  
QY 61 ADVYKGRFTISSDDSKNTAYLQNMNSLRADPTAVYYCTASGYWFAWVGGLVTYSS 116  
DB 61 ADVYKGRFTISGDSDSKNTAYLQNMNSLRADPTAVYYCTTSGYWFAYWVGGLVTYSS 116

RESULT 8  
US-09-910-483-17  
; Sequence 17, Application US/09910483  
; Publication No. US20030035798A1

GENERAL INFORMATION:  
; APPLICANT: FANG, FANG  
; APPLICANT: KOHLSTADT, LORI  
; APPLICANT: RENO, JOHN  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; FILE REFERENCE: 014357/027 8772  
; CURRENT APPLICATION NUMBER: US/09/910,483  
; CURRENT FILING DATE: 2001-07-19  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VH Domain  
; OTHER INFORMATION: peptide of Hum E  
US-09-910-483-17

Query Match 95.5%; Score 589; DB 10; Length 116;  
Best Local Similarity 94.8%; Pred. No. 2.5e-49;  
Matches 110; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTYY 60  
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTYY 60  
QY 61 ADVYKGRFTISSDDSKNTAYLQNMNSLRADPTAVYYCTASGYWFAWVGGLVTYSS 116  
DB 61 DPKVQGRFTISADDSKNTAYLQNMNSLRADPTAVYYCTTSGYWFAYWVGGLVTYSS 116

## RESULT 9

US-09-910-483-29  
; Sequence 29, Application US/09910483  
; Publication No. US20030035798A1  
; GENERAL INFORMATION:  
; APPLICANT: FANG, FANG  
; APPLICANT: KOHLSTADT, LORI  
; APPLICANT: RENO, JOHN  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; FILE REFERENCE: 014357/027 8772  
; CURRENT APPLICATION NUMBER: US/09/910,483  
; CURRENT FILING DATE: 2001-07-19  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VH Domain  
; OTHER INFORMATION: peptide of Hum H  
US-09-910-483-29

Query Match 95.5%; Score 589; DB 10; Length 116;  
Best Local Similarity 94.8%; Pred. No. 2.5e-49;  
Matches 110; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTYY 60  
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFINIKDTYIMHWQAQPGKLEWVARIDPANDNTYY 60  
QY 61 ADVYKGRFTISSDDSKNTAYLQNMNSLRADPTAVYYCTASGYWFAWVGGLVTYSS 116  
DB 61 DPKVQGRFTISADDSKNTAYLQNMNSLRADPTAVYYCTTSGYWFAYWVGGLVTYSS 116

RESULT 10  
US-09-910-483-33  
; Sequence 33, Application US/09910483  
; Publication No. US20030035798A1  
; GENERAL INFORMATION:

APPLICANT: FANG, FANG  
APPLICANT: KOHLSTADT, LORI  
APPLICANT: RENO, JOHN  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
FILE REFERENCE: 014357/027 8772  
CURRENT APPLICATION NUMBER: US/09/910.483  
CURRENT FILING DATE: 2001-07-19  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 33  
LENGTH: 116  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: Description of Artificial Sequence: Synthetic VH Domain  
OTHER INFORMATION: peptide of Hum I  
US-09-910-483-33

Query Match 93.4%; Score 576; DB 10; Length 116;  
Best Local Similarity 92.2%; Pred. No. 4.4e-48;  
Matches 107; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVQAQPGKLEWVARIDPANDNTIY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVQAQPGKLEWVARIDPANDNTIY 60  
QY 61 ADSVKGRTTSSDSDSKNTAYLQMSLRADPTAVYYCTASGTPWYWGGLTVTVSS 116  
DB 61 DPKVQGRFTTSDTSKNTAYLQMSLRADPTAVYYCTTSGWTFWYWGGLTVTVSS 116

RESULT 11  
US-09-971-543-11  
Sequence 11, Application US/09971543  
Patent No. US20020146846A1  
GENERAL INFORMATION:  
APPLICANT: PLUCKTUN, ANDREAS  
APPLICANT: HONEGGER, ANNEMARIE  
APPLICANT: WILHOLD, JORG  
TITLE OF INVENTION: NOVEL METHOD FOR THE STABILIZATION OF CHIMERIC  
TITLE OF INVENTION: IMMUNOGLOBULIN OR IMMUNOGLOBULIN FRAGMENTS, AND  
FILE REFERENCE: PLUCK-3 CON  
CURRENT APPLICATION NUMBER: US/09/971.543  
CURRENT FILING DATE: 2001-10-04  
PRIOR APPLICATION NUMBER: PCT/EP00/03176  
PRIOR FILING DATE: 2000-04-10  
PRIOR APPLICATION NUMBER: EP 99 10 7030.1  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: Description of Artificial Sequence: Synthetic 4DS peptide  
US-09-971-543-11

Query Match 84.0%; Score 518; DB 9; Length 120;  
Best Local Similarity 85.8%; Pred. No. 1.8e-42;  
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVQAQPGKLEWVARIDPANDNTIY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVQAQPGKLEWVARIPYPTNGYTRY 60  
QY 61 ADSVKGRTTSSDSDSKNTAYLQMSLRADPTAVYYCTASG---YMFAYWGGLTVTVSS 116  
DB 61 ADSVKGRTTSSDSDSKNTAYLQMSLRADPTAVYYCTSRMGDGFYANDYWGGLTVTVSS 120

RESULT 12

US-10-411-037-36  
Sequence 36, Application US/10411037  
Publication No. US20040043446A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA  
FILE REFERENCE: 040853-01-5082  
CURRENT APPLICATION NUMBER: US/10/411.037  
CURRENT FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 36  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-411-037-36

Query Match 84.0%; Score 518; DB 12; Length 120;  
Best Local Similarity 85.8%; Pred. No. 1.8e-42;  
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVQAQPGKLEWVARIDPANDNTIY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWVQAQPGKLEWVARIPYPTNGYTRY 60  
QY 61 ADSVKGRTTSSDSDSKNTAYLQMSLRADPTAVYYCTASG---YMFAYWGGLTVTVSS 116  
DB 61 ADSVKGRTTSSDSDSKNTAYLQMSLRADPTAVYYCTSRMGDGFYANDYWGGLTVTVSS 120

RESULT 13

US-10-411-026-36  
Sequence 36, Application US/10411026  
Publication No. US20040063911A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE  
FILE REFERENCE: 040853-01-5053  
CURRENT APPLICATION NUMBER: US/10/411.026  
CURRENT FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07

PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 36  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-411-026-36

Query Match 84.0%; Score 518; DB 12; Length 120;  
Best Local Similarity 85.8%; Pred. No. 1.8e-42;  
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWYRQAPGKLEWVARIDPANDNTIY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWYRQAPGKLEWVARIPYPTNGYTRY 60  
QY 61 ADSYKGRFTISSDSKNTAYIQMNSLRADPTAVYYCTASG---YMFAYMGQGLLVTVSS 116  
DB 61 ADSYKGRFTISADTSKNTAYIQMNSLRADPTAVYYCSRWDGDFYAMDYMGQGLLVTVSS 120

RESULT 14  
US-10-410-894-2  
Sequence 2, Application US/10410894  
Publication No. US20030228663A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: LOWMAN, Henry B.  
APPLICANT: GERSTNER, Reel B.  
APPLICANT: CARTER, Paul J.  
TITLE OF INVENTION: ANTI-HER2 ANTIBODY VARIANTS  
FILE REFERENCE: 39766-0108 US  
CURRENT APPLICATION NUMBER: US/10/410,894  
CURRENT FILING DATE: 2003-04-09  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 120  
TYPE: PRT  
ORGANISM: homo sapiens  
US-10-410-894-2

Query Match 84.0%; Score 518; DB 15; Length 120;  
Best Local Similarity 85.8%; Pred. No. 1.8e-42;  
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWYRQAPGKLEWVARIDPANDNTIY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWYRQAPGKLEWVARIPYPTNGYTRY 60  
QY 61 ADSYKGRFTISSDSKNTAYIQMNSLRADPTAVYYCTASG---YMFAYMGQGLLVTVSS 116  
DB 61 ADSYKGRFTISADTSKNTAYIQMNSLRADPTAVYYCSRWDGDFYAMDYMGQGLLVTVSS 120

RESULT 15  
US-10-410-962-36  
Sequence 36, Application US/10410962  
Publication No. US2004007836A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Deftrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Hakes, David

APPLICANT: Chen, Xi  
APPLICANT: Bove, Caryn  
TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND  
TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF  
FILE REFERENCE: 040853-01-5054  
CURRENT APPLICATION NUMBER: US/10/410,962  
CURRENT FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 36  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-410-962-36

Query Match 84.0%; Score 518; DB 16; Length 120;  
Best Local Similarity 85.8%; Pred. No. 1.8e-42;  
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWYRQAPGKLEWVARIDPANDNTIY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYIHWYRQAPGKLEWVARIPYPTNGYTRY 60  
QY 61 ADSYKGRFTISSDSKNTAYIQMNSLRADPTAVYYCTASG---YMFAYMGQGLLVTVSS 116  
DB 61 ADSYKGRFTISADTSKNTAYIQMNSLRADPTAVYYCSRWDGDFYAMDYMGQGLLVTVSS 120

Search completed: May 13, 2004, 17:34:31  
Job time : 190.857 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:43:32 ; Search time 21.2143 Seconds  
(without alignments)  
265.084 Million cell updates/sec

Title: US-09-910-483-7

Perfect score: 566  
Sequence: 1 DIOMTQSPSSLSASVGDRT.....QQSNMPTFGGQTKYKIR 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465	82.2	108	KV1V_HUMAN	P04430 homo sapien
2	463	81.8	108	KV1H_HUMAN	P01600 homo sapien
3	461	81.4	108	KV1G_HUMAN	P01599 homo sapien
4	460	81.3	108	KV1R_HUMAN	P01605 homo sapien
5	458	80.9	108	KV1R_HUMAN	P01610 homo sapien
6	457	80.7	129	KV1W_HUMAN	P04431 homo sapien
7	450	79.5	108	KV1B_HUMAN	P01594 homo sapien
8	448	79.2	108	KV1E_HUMAN	P01597 homo sapien
9	446	78.8	108	KV1O_HUMAN	P01607 homo sapien
10	444	78.4	108	KV1N_HUMAN	P01606 homo sapien
11	442	78.1	108	KV1P_HUMAN	P01608 homo sapien
12	442	78.1	108	KV1E_HUMAN	P01611 homo sapien
13	441	77.9	108	KV1F_HUMAN	P01598 homo sapien
14	440	77.7	108	KV1L_HUMAN	P01604 homo sapien
15	439.5	77.7	107	KV1D_HUMAN	P01596 homo sapien
16	438	77.4	108	KV1C_HUMAN	P01595 homo sapien
17	438	77.4	108	KV1Y_HUMAN	P01602 homo sapien
18	429	75.8	108	KV1A_HUMAN	P01593 homo sapien
19	427	75.4	108	KV1X_HUMAN	P01603 homo sapien
20	426	75.3	108	KV1O_HUMAN	P01601 homo sapien
21	422	74.6	129	KV1X_HUMAN	P04432 homo sapien
22	419.5	74.1	129	KV3H_HUMAN	P04207 homo sapien
23	416.5	73.6	109	KV1T_HUMAN	P01612 homo sapien
24	414	73.1	107	KV1J_HUMAN	P01602 homo sapien
25	408	72.1	108	KV5K_MOUSE	P01644 mus musculu
26	407	71.9	117	KV1I_HUMAN	P01604 mus musculu
27	405.5	71.6	109	KV3F_HUMAN	P01624 homo sapien
28	403	71.2	108	KV5L_MOUSE	P01645 mus musculu
29	403	71.2	108	KV5O_MOUSE	P01648 mus musculu
30	402.5	71.1	109	KV3D_HUMAN	P01622 homo sapien
31	399.5	70.6	109	KV3B_HUMAN	P01620 homo sapien
32	399	70.5	108	KV5S_MOUSE	P01652 mus musculu
33	398.5	70.4	129	KV3M_HUMAN	P18136 homo sapien

34	398	70.3	108	1	KV5J_MOUSE	P01643 mus musculu
35	398	70.3	108	1	KV5M_MOUSE	P01646 mus musculu
36	398	70.3	108	1	KV5P_MOUSE	P01649 mus musculu
37	397.5	70.2	129	1	KV3J_HUMAN	P18135 homo sapien
38	396	70.0	108	1	KV5N_HUMAN	P01647 mus musculu
39	396	70.0	108	1	KV5Q_MOUSE	P01650 mus musculu
40	395	69.8	114	1	KV4A_HUMAN	P01625 homo sapien
41	395	69.8	134	1	KV4C_HUMAN	P06314 homo sapien
42	392	69.3	108	1	KV5T_MOUSE	P01653 mus musculu
43	391.5	69.2	109	1	KV3E_HUMAN	P01623 homo sapien
44	390	68.9	108	1	KV5D_MOUSE	P01636 mus musculu
45	388	68.6	108	1	KV5U_MOUSE	P04946 mus musculu

ALIGNMENTS

RESULT 1	ID	KV1V_HUMAN	STANDARD;	PRT;	108 AA.
AC	P04430	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, last sequence update)				
DE	15-JUL-1999 (Rel. 38, last annotation update)				
DE	Ig kappa chain V-I region BAN.				
OS	Homo sapiens (Human)				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=66174817; Pubmed=3083240;				
RA	Dwulet F.E., O'Connor T.P., Benson M.D.;				
RT	"Polymorphism in a kappa I primary (AI) amyloid protein (BAN).";				
RL	Mol. Immunol. 23:73-78(1986).				
DR	PIR; A01878; KIHUEN.				
DR	HSSP; P80362; 1WTU.				
DR	GO; GO:0005576; C:extracellular; NAS.				
DR	GO; GO:0003823; P:antigen binding; NAS.				
DR	GO; GO:0006955; P:immune response; NAS.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
KW	Immunoglobulin V region; Amyloid.				
FT	DOMAIN 1 23				
FT	DOMAIN 24 34				
FT	DOMAIN 35 49				
FT	DOMAIN 50 56				
FT	DOMAIN 57 86				
FT	DOMAIN 89 97				
FT	DOMAIN 98 107				
FT	DISULFID 23 88				
FT	NON TER 108				
SO	SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;				
Query Match	82.2%; Score 465; DB 1; Length 108;				
Best Local Similarity	83.3%; Pred. No. 8,7e-41;				
Matches	90; Conservative 7; Mismatches 11; Indels 0; Gaps 0;				
Qy	1 DIOMTQSPSSLSASVGDRTTCRASOSISNLMHWQKGRKAPKLIYHASOSISGVPS 60				
Db	1 DIQITQSPSSLSASVGRVTTCASOSVYNYVAMFOQKGRKAKSLIYDASTLOSQVPS 60				
Qy	61 RFSSGGSGTDFTLTSSLOPEDFATYCCOOSNMPYTFGGQTKYKIR 108				
Db	61 NFGSSGSGTDFILTLSSLOPEDFATYCCQXNSYPTFGGQTKYKIR 108				
RESULT 2	KV1H_HUMAN	STANDARD;	PRT;	108 AA.	

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AC POL600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=71032830; PubMed=4097974;
RA Metanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups."
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR HSP; A01868; K1H0U.
DR HSP; P80362; 1WT.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160BD0618 CRC64;

Query Match 81.8%; Score 463; DB 1; Length 108;
Best Local Similarity 85.2%; Pred. No. 1,4e-40;
Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTGSPSSLSASVGDRTVITTCRASQSIENNIMHWYQKRGKAPKLLIYASQISGVPS 60
DB 1 DIQMTGSPSSLSASVGDRTVITTCRASQSIENNIMHWYQKRGKAPKLLIYASQISGVPS 60
QY 61 RFGSGSGGTDFTLTISLSLOPEDPATYTCQNSNMPYFGGTVEIKR 108
DB 61 RFGSGSGGTDFTLTISLSLOPEDPATYTCQNSNMPYFGGTVEIKR 108

RESULT 3
KVIG HUMAN STANDARD; PRT; 108 AA.
ID P01599;
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Gal.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal Igm-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I."

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RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504 (1973).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01867; K1H0U.
DR HSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; IG LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FE73 CRC64;

Query Match 81.4%; Score 461; DB 1; Length 108;
Best Local Similarity 84.3%; Pred. No. 2,2e-40;
Matches 91; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTGSPSSLSASVGDRTVITTCRASQSIENNIMHWYQKRGKAPKLLIYASQISGVPS 60
DB 1 DIQMTGSPSSLSASVGDRTVITTCRASQGIENIDLTWYQKRGKAPKLLIYASQISGVPS 60
QY 61 RFGSGSGGTDFTLTISLSLOPEDPATYTCQNSNMPYFGGTVEIKR 108
DB 61 RFGSGSGGTDFTLTISLSLOPEDPATYTCQNSNMPYFGGTVEIKR 108

RESULT 4
KVIM HUMAN STANDARD; PRT; 108 AA.
ID P01605;
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT Igm anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities."
RL Scand. J. Immunol. 5:677-684 (1976).
CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-ITI KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01871; K1H0U.
DR HSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.

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DR PROSITE; PS50835; IG LIKE; 1.  
KM Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;  
Query Match 81.3%; Score 460; DB 1; Length 108;  
Best Local Similarity 81.5%; Pred. No. 2.8e-40;  
Matches 88; Conservative 8; Mismatches 12; Indels 0; Gaps 0;  
Db 61 RFSGSGGTDFLTITSLQPEDPATYTCQGSNSWPTFGGTKEIKR 108  
QY 1 DIQWTQSPSSLSASVGRVITTCRASQISNNLHMVQOKRGKAPKLLIYASQISGVPS 60  
1 DIQWTQSPSSLSASVGRVITTCRASQISNNLHMVQOKRGKAPKLLIYASQISGVPS 60  
DB 61 RFSGSGGTDFLTITSLQPEDPATYTCQGSNSWPTFGGTKEIKR 108  
61 RFSGSGGTDFLTITSLQPEDPATYTCQGSNSWPTFGGTKEIKR 108  
RESULT 5  
KVIR\_HUMAN STANDARD; PRT; 108 AA.  
ID KVIR\_HUMAN P01610;  
AC P01610;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region WEA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=63273707; PubMed=6410398;  
RA Goni F., Frangione B.;  
RT "Amino acid sequence of the Fv region of a human monoclonal IGM  
RT (proteose WEA) with antibody activity against 3,4-pyruvylated  
RT galactose in Klebsiella polysaccharides K30 and K33.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).  
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH  
CC WALDENSTROM'S MACROGLOBULINEMIA.  
DR PIR; A01876; KIHUWE.  
DR HSSP; P80362; IWTU.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IG\_1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KM Immunoglobulin V region; Monoclonal antibody.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11840 MW; 9249861F0945618C CRC64;  
Query Match 80.9%; Score 458; DB 1; Length 108;  
Best Local Similarity 82.4%; Pred. No. 4.5e-40;

Matches 89; Conservative 8; Mismatches 11; Indels 0; Gaps 0;  
QY 1 DIQWTQSPSSLSASVGRVITTCRASQISNNLHMVQOKRGKAPKLLIYASQISGVPS 60  
1 DIQWTQSPSSLSASVGRVITTCRASQISNNLHMVQOKRGKAPKLLIYASQISGVPS 60  
DB 61 RFSGSGGTDFLTITSLQPEDPATYTCQGSNSWPTFGGTKEIKR 108  
61 RFSGSGGTDFLTITSLQPEDPATYTCQGSNSWPTFGGTKEIKR 108  
RESULT 6  
KVIR\_HUMAN STANDARD; PRT; 129 AA.  
ID KVIR\_HUMAN P04431;  
AC P04431;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Walker precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85014148; PubMed=6091049;  
RA Klobbeck H.G., Combratio G., Zachau H.G.;  
RT "Immunoglobulin genes of the kappa light chain type from two human  
RT lymphoid cell lines are closely related.";  
RL Nucleic Acids Res. 12:6995-7006(1984).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC -----  
DR EMBL; X00965; CA25477.1; ALT\_TERM.  
DR PIR; A01883; KIHUWK.  
DR HSSP; P01607; IREI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IG\_1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KM Immunoglobulin V region; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.  
FT DOMAIN 23 45 FRAMEWORK-1.  
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 57 71 FRAMEWORK-2.  
FT DOMAIN 72 78 FRAMEWORK-3.  
FT DOMAIN 79 110 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 111 119 FRAMEWORK-3.  
FT DOMAIN 120 129 COMPLEMENTARITY-DETERMINING-3.  
FT DISULFID 45 110 BY SIMILARITY.  
FT NON TER 129 129  
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC29 CRC64;  
Query Match 80.7%; Score 457; DB 1; Length 129;  
Best Local Similarity 86.9%; Pred. No. 7e-40;  
Matches 93; Conservative 3; Mismatches 11; Indels 0; Gaps 0;  
QY 1 DIQWTQSPSSLSASVGRVITTCRASQISNNLHMVQOKRGKAPKLLIYASQISGVPS 60  
1 DIQWTQSPSSLSASVGRVITTCRASQISNNLHMVQOKRGKAPKLLIYASQISGVPS 60  
DB 61 RFSGSGGTDFLTITSLQPEDPATYTCQGSNSWPTFGGTKEIKR 107  
61 RFSGSGGTDFLTITSLQPEDPATYTCQGSNSWPTFGGTKEIKR 107

Db 83 RFGSGSGTDFLTITSLQPEDSATYCCQGSYSLTFITFGQTRLEIK 129

## RESULT 7

KV1B HUMAN STANDARD; PRT; 108 AA.

AC P01594;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig kappa chain V-I region AU.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72189444; PubMed=5028201;  
RA Schiehl H., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
protein Au).";  
RT Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).  
RN [2]  
RN X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE=77022433; PubMed=1234024;  
RA Fehlbauer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
RT "The structure determination of the variable portion of the  
Bence-Jones protein Au.";  
RT Biophys. Struct. Mech. 1:139-146(1975).  
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY  
MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V  
REGION OF THE KAPPA CHAIN REI.  
CC -1- MISCELLANEOUS: THIS C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -1- MISCELLANEOUS: THIS IS A Bence-Jones protein.  
DR PIR; A91653; KIHUAV.  
DR PDB; 1JVS; 30-JAN-02.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 2 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 3 35 49 FRAMEWORK-2.  
FT DOMAIN 4 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 5 57 88 FRAMEWORK-3.  
FT DOMAIN 6 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 7 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6B9 CRC64;

Query Match 79.5%; Score 450; DB 1; Length 108;  
Best Local Similarity 82.4%; Pred. No. 3e-39;  
Matches 89; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIOMTSPSSLSASVGDRTITCRASOSISNNLHWYQOKGKAPKLLIYHASOSISGVS 60  
Db 1 DIOMTSPSSLSASVGDRTITCRASODISDYIMWYQOKGKAPKLLIYDASNLSEGVPS 60  
QY 61 RFGSGSGTDFLTITSLQPEDPATYCCQGSNSWPYTFGQTRVEIKR 108  
Db 61 RFGSGSGAHFTITSLQPEDPATYCCQGYDVLPTPTFGQTRVEIKR 108

RESULT 8

KV1E HUMAN STANDARD; PRT; 108 AA.

AC P01597;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region DEE.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72053133; PubMed=5124396;  
RA Milstein C.P., Deverson E.V.;  
RT "The amino acid sequence of a human kappa light chain.";  
RL Biochem. J. 123:945-958(1971).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
DR PIR; A01865; KIHUDE.  
DR HSP; P01607; IREI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 2 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 3 35 49 FRAMEWORK-2.  
FT DOMAIN 4 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 5 57 88 FRAMEWORK-3.  
FT DOMAIN 6 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 7 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11661 MW; BDDE6350017F1E51 CRC64;

Query Match 79.2%; Score 448; DB 1; Length 108;  
Best Local Similarity 79.6%; Pred. No. 4.8e-39;  
Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIOMTSPSSLSASVGDRTITCRASOSISNNLHWYQOKGKAPKLLIYHASOSISGVS 60  
Db 1 BIZMTSPSSLSASVGDRTITCRAGOSVKNLWYQOKGKAPKLLIYFAASLSGVS 60  
QY 61 RFGSGSGTDFLTITSLQPEDPATYCCQGSNSWPYTFGQTRVEIKR 108  
Db 61 RFGSGSGTDFLTITSLQPEDPATYCCQSYTTPTPTFGQTRVEIKR 108

## RESULT 9

KV1O HUMAN STANDARD; PRT; 108 AA.

AC P01607;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig kappa chain V-I region Rel.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=76023758; PubMed=809329;  
RA Palm W., Hilschmann N.;  
RT "The primary structure of a crystalline monoclonal immunoglobulin  
kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation  
and characterization of the tryptic peptides; the complete amino acid  
sequence of the protein; a contribution to the elucidation of the

RT three-dimensional structure of antibodies, in particular their  
 RT combining site." ;  
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=7603966; Pubmed=1182131;  
 RA Bep O., Latman E.E., Schiffer M., Huber R., Palm W.;  
 RT "The molecular structure of a dimer composed of the variable portions  
 of the Bence-Jones protein REI refined at 2.0-A resolution." ;  
 RL Biochemistry 14:4943-4952(1975).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
 CC MARKER.  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 CC PIR; A91663; KIHURE.  
 DR PDB; 1RE1; 17-FEB-84.  
 DR PDB; 1AR2; 12-NOV-87.  
 DR PDB; 1BMW; 29-DEC-99.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
 KW DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 1 23 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88  
 FT STRAND 4 7  
 FT TURN 10 13  
 FT TURN 15 16  
 FT STRAND 19 25  
 FT TURN 30 31  
 FT STRAND 33 38  
 FT TURN 40 41  
 FT STRAND 44 49  
 FT TURN 50 52  
 FT STRAND 53 54  
 FT TURN 56 57  
 FT TURN 60 61  
 FT STRAND 62 67  
 FT TURN 68 69  
 FT STRAND 70 75  
 FT HELIX 80 82  
 FT STRAND 85 90  
 FT STRAND 97 98  
 FT STRAND 102 106  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11902 MW; 9E8143E118BCE2A CRC64;  
 Query Match 78.8%; Score 446; DB 1; Length 108;  
 Best Local Similarity 80.6%; Pred. No. 7.6e-39;  
 Matches 87; Conservative 6; Mismatches 15; Indels 0; Gaps 0;  
 Db 1 DIQWTSPPSSLSASVGRVITTCRASOSISNNLHWYQOKPKAKLIIYASOSISGVPS 60  
 1 DIQWTSPPSSLSASVGRVITTCRASODIIKYLWYQOTPEKAKLIIYASNNIAGVPS 60  
 QY RFGSGSGTDTFTLTISLQPEDPATYVYCOQSNMWPTFGGQTKVEIKR 108  
 61 RFGSGSGTDTYFTLTISLQPEDATYVYCOQYQSLPYTFGGQTKQLITR 108  
 Db 61 RFGSGSGTDTYFTLTISLQPEDATYVYCOQYQSLPYTFGGQTKQLITR 108  
 ID KVIP HUMAN STANDARD; PRT; 108 AA.  
 AC P01606;  
 RESULT 10  
 ID KVIN HUMAN  
 AC P01606;  
 STANDARD; PRT; 108 AA.

DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region OU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=70201507; Pubmed=547531;  
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;  
 RT "Macroglobulin structure: variable sequence of light and heavy  
 chains." ;  
 RL Science 169:56-59(1970).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
 CC MACROGLOBULIN.  
 CC PIR; A01872; KIHUOU.  
 DR HSSP; P01607; 1REI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; IgV; 1.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11777 MW; 8283DA24105827E CRC64;  
 Query Match 78.4%; Score 444; DB 1; Length 108;  
 Best Local Similarity 74.1%; Pred. No. 1.2e-38;  
 Matches 80; Conservative 17; Mismatches 11; Indels 0; Gaps 0;  
 Db 1 DIQWTSPPSSLSASVGRVITTCRASOSISNNLHWYQOKPKAKLIIYASOSISGVPS 60  
 1 DIQWTSPPSSLSASVGRVITTCRASZTISYLBWYZKKPKABLLIYASBLHSGVPS 60  
 QY RFGSGSGTDTFTLTISLQPEDPATYVYCOQSNMWPTFGGQTKVEIKR 108  
 61 RFGSGSGTDTFTLTISLQPEDPATYVYCOQSNMWPTFGGQTKVEIKR 108  
 Db 61 RFGSGSGTDTFTLTISLQPEDPATYVYCOQSNMWPTFGGQTKVEIKR 108  
 ID KVIP HUMAN STANDARD; PRT; 108 AA.  
 AC P01606;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Roy.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=68362076; Pubmed=5595110;  
 RA Hilschmann N.;  
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and  
 Cum.)." ;  
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).  
 RN [2]

RP REVISIONS TO 39 AND 41.  
 RA Hilschmann N., Barnikol H.U., Hees M., Langer B., Ponstingl H.,  
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;  
 RL (in) Frank F., Shugar D. (eds.);  
 RL Gamma globulins: structure and function, pp.57-74, Academic Press,  
 New York (1969).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
 CC MARKER.  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 DR PIR: A91638; KIHURY.  
 DR HSSP: P80362; IWTU.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11782 MW; F5ACEDESA313DF3A CRC64;  
 Query Match 78.1%; Score 442; DB 1; Length 108;  
 Best Local Similarity 80.6%; Pred. No. 1.9e-38;  
 Matches 87; Conservative 8; Mismatches 13; Indels 0; Gaps 0;  
 Db 61 RFGSGSGTDFLTITISLQPEDPATYTCQOQNSMPTFGGTVEIKR 108  
 QY 1 D1QMTQSPSSLSASVGRVITTCRASQISNNLHWYQQRGKAPKLLIYASQISGVPS 60  
 DB 1 D1QMTQSPSSLSASVGRVITTCRASQISNNLHWYQQRGKAPKLLIYASQISGVPS 60  
 QY 61 RFGSGSGTDFLTITISLQPEDPATYTCQOQNSMPTFGGTVEIKR 108  
 DB 61 RFGSGSGTDFLTITISLQPEDPATYTCQOQNSMPTFGGTVEIKR 108  
 Db 61 RFGSGSGTDFLTITISLQPEDPATYTCQOQNSMPTFGGTVEIKR 108  
 RESULT 12  
 KVIS\_HUMAN STANDARD; PRT; 108 AA.  
 ID KVIS\_HUMAN  
 AC P01611;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Web.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE.  
 RX MEDLINE=81092279; PubMed=677806;  
 RA Kratin H., Yang C., Krusche J.U., Hilschmann N.;  
 RT "Preparative separation of the tryptic hydrolysate of a protein by  
 RT high-pressure liquid chromatography. The primary structure of a  
 RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein  
 RT Web).";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598 (1980).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 DR PIR: A01877; KIHUMS.  
 DR HSSP: P80362; IWTU.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E845 CRC64;  
 Query Match 78.1%; Score 442; DB 1; Length 108;  
 Best Local Similarity 81.5%; Pred. No. 1.9e-38;  
 Matches 88; Conservative 8; Mismatches 12; Indels 0; Gaps 0;  
 Db 61 RFGSGSGTDFLTITISLQPEDPATYTCQOQNSMPTFGGTVEIKR 108  
 QY 1 D1QMTQSPSSLSASVGRVITTCRASQISNNLHWYQQRGKAPKLLIYASQISGVPS 60  
 DB 1 D1QMTQSPSSLSASVGRVITTCRASQISNNLHWYQQRGKAPKLLIYASQISGVPS 60  
 QY 61 RFGSGSGTDFLTITISLQPEDPATYTCQOQNSMPTFGGTVEIKR 108  
 DB 61 RFGSGSGTDFLTITISLQPEDPATYTCQOQNSMPTFGGTVEIKR 108  
 Db 61 RFGSGSGTDFLTITISLQPEDPATYTCQOQNSMPTFGGTVEIKR 108  
 RESULT 13  
 KVIS\_HUMAN STANDARD; PRT; 108 AA.  
 ID KVIS\_HUMAN  
 AC P01558;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region EU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE.  
 RX MEDLINE=71064023; PubMed=5489770;  
 RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino  
 RT acid sequence of the light chain.";  
 RL Biochemistry 9:3155-3161 (1970).  
 [2]  
 RP DISULFIDE BOND.  
 RX MEDLINE=71064027; PubMed=4923144;  
 RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 RT Intrachain disulfide bonds.";  
 RL Biochemistry 9:3168-3196 (1970).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 DR PIR: A90562; KIHURU.  
 DR HSSP: P01607; IRET.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2P4B88923 CRC64;

Query Match 77.9%; Score 441; DB 1; Length 108;  
 Best Local Similarity 82.2%; Pred. No. 2.5e-38;  
 Matches 88; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQWTOSSSLASVGDRTVITTCRASOSISNNLHWYQKPKKLIYHASOSISGVPS 60  
 DB 1 DIQWTOSSPTLSASVGRVITTCRASOSINTWLMWYQKPKKLIYKASISLESVPS 60

QY 61 RFGSGSGTDTFTLTISLQPEDPATYVYCOQNSMWPYFGQTKVEIKR 107  
 DB 61 RFGSGSGTDTFTLTISLQPEDPATYVYCOQNSMWPYFGQTKVEIKR 107

## RESULT 14

ID\_KVID\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01604;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Kue.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NX NCBI\_Taxid=9606;  
 RN [1]

RP SEQUENCE  
 MEDLINE=79237924; PubMed=112021;  
 RA Eulitz M., Kley H.-P., Zeidler H.-J.;  
 RT "The primary structure of the Bence-Jones protein Kue. The amino acid  
 sequence of the variable part of a human L-chain of the kappa-type.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.

DR PIR; A01870; KIHUKU.  
 DR HSSP; P01607; IREI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4B98 CRC64;

Query Match 77.7%; Score 440; DB 1; Length 108;  
 Best Local Similarity 79.6%; Pred. No. 3.1e-38;  
 Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTOSSSLASVGDRTVITTCRASOSISNNLHWYQKPKKLIYHASOSISGVPS 60  
 DB 1 DIQWTOSSPTLSASVGRVITTCRASOSINTWLMWYQKPKKLIYKASISLESVPS 60

QY 61 RFGSGSGTDTFTLTISLQPEDPATYVYCOQNSMWPYFGQTKVEIKR 108  
 DB 61 RFGSGSGTDTFTLTISLQPEDPATYVYCOQNSMWPYFGQTKVEIKR 108

## RESULT 15

ID\_KVID\_HUMAN STANDARD; PRT; 107 AA.  
 AC P01596;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region CAR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NX NCBI\_Taxid=9606;  
 RN [1]

RP SEQUENCE  
 MEDLINE=75075135; PubMed=4216454;  
 RA Mistein C.P., Deverson E.V.;  
 RT "Primary structure of kappa light chain from a human myeloma  
 protein.";  
 RL Eur. J. Biochem. 49:377-391(1974).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

DR PIR; A01864; KIHUAR.  
 DR HSSP; P80362; IWTU.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region; Glycoprotein.  
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).  
 FT NON TER 107 107  
 SQ SEQUENCE 107 AA; 11703 MW; E1BFD0P9844C346 CRC64;

Query Match 77.7%; Score 439.5; DB 1; Length 107;  
 Best Local Similarity 79.6%; Pred. No. 3.5e-38;  
 Matches 86; Conservative 12; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIQWTOSSSLASVGDRTVITTCRASOSISNNLHWYQKPKKLIYHASOSISGVPS 60  
 DB 1 DIQWTOSSPTLSASVGRVITTCRASOSISNNLHWYQKPKKLIYKASISLESVPS 60

QY 61 RFGSGSGTDTFTLTISLQPEDPATYVYCOQNSMWPYFGQTKVEIKR 108  
 DB 61 RFGSGSGTDTFTLTISLQPEDPATYVYCOQNSMWPYFGQTKVEIKR 107

Search completed: May 13, 2004, 16:57:24  
 Job time : 21.2143 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:43:32 ; Search time 22.7857 Seconds  
(without alignments)  
265.084 Million cell updates/sec

Title: US-09-910-483-5

Perfect score: 617  
Sequence: 1 EVGLVSGGGLVQPGGSLRL.....TAGGYFAVYWGQGLTVVSS 116

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	421.5	68.3	115	1	HV3D_HUMAN
2	421	68.2	122	1	HV3G_HUMAN
3	420.5	68.2	119	1	HV3I_HUMAN
4	412.5	66.9	115	1	HV3J_MOUSE
5	411	66.6	114	1	HV3B_HUMAN
6	406	65.8	116	1	HV3I_HUMAN
7	405.5	65.7	113	1	HV3H_HUMAN
8	405.5	65.7	113	1	HV3J_MOUSE
9	405.5	65.7	113	1	HV3I_MOUSE
10	404.5	65.6	113	1	HV3I_MOUSE
11	402.5	65.2	142	1	HV01_RAT
12	401.5	65.1	115	1	HV3J_MOUSE
13	401	65.0	136	1	HV16_MOUSE
14	399.5	64.7	136	1	HV28_MOUSE
15	398	64.5	120	1	HV3U_HUMAN
16	398	64.5	122	1	HV3A_HUMAN
17	397.5	64.4	121	1	HV3U_HUMAN
18	395.5	64.1	113	1	HV29_MOUSE
19	395.5	64.1	120	1	HV3E_HUMAN
20	394.5	63.9	115	1	HV3F_HUMAN
21	394.5	63.9	119	1	HV3L_HUMAN
22	393	63.7	119	1	HV3M_HUMAN
23	389	63.0	119	1	HV3T_MOUSE
24	389	63.0	119	1	HV3N_HUMAN
25	389	63.0	122	1	HV21_MOUSE
26	386.5	62.6	123	1	HV18_MOUSE
27	385.5	62.5	116	1	HV05_CARAU
28	385	62.4	114	1	HV01_CANPA
29	384.5	62.3	117	1	HV17_MOUSE
30	384	62.2	117	1	HV3C_HUMAN
31	383	62.1	119	1	HV3B_HUMAN
32	383	62.1	119	1	HV3P_HUMAN
33	382.5	62.0	123	1	HV19_MOUSE

34	382	61.9	119	1	HV40_MOUSE	P01810 mus musculus
35	381.5	61.8	123	1	HV25_MOUSE	P01794 mus musculus
36	381	61.8	126	1	HV2K_HUMAN	P01772 homo sapien
37	379.5	61.5	123	1	HV22_MOUSE	P01781 mus musculus
38	379.5	61.5	123	1	HV24_MOUSE	P01793 mus musculus
39	377.5	61.2	123	1	HV23_MOUSE	P01792 mus musculus
40	377	61.1	117	1	HV3O_HUMAN	P01776 homo sapien
41	375.5	60.9	117	1	HV3O_MOUSE	P01812 mus musculus
42	375	60.8	111	1	HV35_MOUSE	P01804 mus musculus
43	373.5	60.5	118	1	HV39_MOUSE	P01809 mus musculus
44	373	60.5	122	1	HV20_MOUSE	P01789 mus musculus
45	369.5	59.9	144	1	HV26_MOUSE	P01795 mus musculus

## ALIGNMENTS

RESULT 1					
ID	HV3D_HUMAN	STANDARD	PRT	115 AA	
AC	P01765	1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Ig heavy chain V-II region TIL.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=78005528; PubMed=409716;				
RA	Wang A.-C., Wang I.Y., Rudenberg H.H.;				
RT	"Immunoglobulin structure and genetics. Identity between variable				
RT	regions of a mu and a gamma2 chain."				
RL	J. Biol. Chem. 252:7192-7199 (1977).				
CC	-I- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS				
CC	OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL				
CC	GAMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO				
CC	IDENTICAL.				
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.				
DR	PIR; A02048; H3HUTL.				
DR	HSSP; P01772; 2P84.				
DR	GO: GO:0005576; C:extracellular; NAS.				
DR	GO: GO:0003823; F:antigen binding; NAS.				
DR	GO: GO:0006955; P:immune response; NAS.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00406; Igv; 1.				
DR	PROSITE; PS50835; IG LIKE; 1.				
KW	Immunoglobulin V region.				
FT	DOMAIN 1 108 IG-LIKE.				
FT	NON TER 115				
SQ	SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;				
Query Match 68.3%; Score 421.5; DB 1; Length 115;					
Best Local Similarity 70.6%; Pred. No. 1.3e-36;					
Matches 84; Conservative 9; Mismatches 19; Indels 7; Gaps 2;					
QY	1 EVGLVSGGGLVQPGGSLRLSCAAGFNIKDTYIHVYRQAPGKLEWVARIDPANDTIY 60				
DB	1 EVGLVSGGGLVQPGGSLRLSCAAGFTFTYVMSVYRQAPGKLZVNGAIZGLSVSZSY 60				
QY	61 ADSYKGRFTISDDSKNTAVLQNSLRADDTAVYYCT--ASGYFAVYWGQGLTVVSS 116				
DB	61 ABSYKGRFTISDDSKNTAVLQNSLRADDTAVYYCT--ASGYFAVYWGQGLTVVSS 115				
RESULT 2					
ID	HV3G_HUMAN	STANDARD;	PRT;	122 AA.	
AC	P01768;				

Query Match.  
Best Local Similarity 68.2%; Score 421; DB 1; Length 122;  
Matches 82; Conservative 13; Mismatches 21; Indels 6; Gaps 2

Dt 21-JUL-1986 (Rel. 01, Last sequence update)  
Dt 21-JUL-1986 (Rel. 01, Last sequence update)  
Dt 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-IIr region CAM.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=81013859; PubMed=6774332;  
RA Lehman D.W., Putnam F.W.;  
RT "Amino acid sequence of the variable region of a human mu chain:  
RT location of a possible JH segment";  
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).  
CC -I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A  
CC PATIENT WITH MACROGLOBULINEMIA.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A02051; MHDMU.  
DR HSSP; P01772; 2FB4.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; P:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SMO0406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
DR Immunoglobulin V region; Pyrrrolidone carboxylic acid.  
KW KX IMUNOGLOBULIN V REGION; PYRROLIDONE CARBOXYLIC ACID.  
FT FT MOD\_RES 1 112  
FT NON\_TER 1 122  
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252FC2 CRC64;

Query Match.  
Best Local Similarity 67.2%; Score 421; DB 1; Length 122;  
Matches 82; Conservative 13; Mismatches 21; Indels 6; Gaps 2

Dt 21-JUL-1986 (Rel. 01, Last sequence update)  
Dt 21-JUL-1986 (Rel. 01, Last sequence update)  
Dt 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-IIr region CAM.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=77070269; PubMed=826475;  
RA Ponstingl H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a  
RT monoclonal IgG1 immunoglobulin (myeloma protein Nle). III. The  
RT chymotryptic peptides of the H-chain, alignment of the tryptic  
RT peptides and discussion of the complete structure.";  
RT Hoppe-Seyster Z. Physiol. Chem. 357:1571-1604(1976).  
RN [2]

RP	DISTUFIDE BOND.
RX	MEDLINE=7070267; PubMed=1002129;
RA	Drexler L., Schwarz U., Reichel W., Hilschmann N.;
RT	"Rule of antibody structure. The primary structure of a monoclonal
RT	IgG1 immunoglobulin (myeloma protein Nle), I: Purification and
RT	characterization of the protein, the L- and H-chains, the
RL	Cyanogen bromide cleavage products, and the disulfide bridges.";
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IgG1 MYELOMA PROTEIN.
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR	PIR; A9168; G1HUNI.
DR	HSSP; P01772; 2FB4.
DR	GO; GO:0005576; C:extracellular; NAS.
DR	GO; GO:0003823; F:antigen binding; NAS.
DR	GO; GO:0006955; P:immune response; NAS.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig_1.
DR	SMART; SMO0406; IGv; 1.
DR	PROSITE; PS50835; IG LIKE; 1.
KW	Immunoglobulin V region; Pyroglutamate carboxylic acid.
FT	DOMAIN 1 112
FT	MOD RES 1 1
FT	DISTUFD 22 96 PYRROLIDONE CARBOXYLIC ACID.
FT	NON_TER 119 119
SQ	SEQUENCE 119 AA; 13242 MW; C96935A6E55E165B CRC64;
Query Match 68.2%; Score 420.5; DB 1; Length 119;	
Best Local Similarity 69.7%; Pred. No. 1.7e-36;	
Matches 83; Conservative 10; Mismatches 23; Indels 3; Gaps 1.	
OY	1 EVLVESGGGLVPGSGSLRLSCAASGFNIKDTYIHWVAQGKGLEWVARIDPANNTY 60
DB	1 QOVIVSGGGVQCGRSRLSCAASGFIFSRYTIIHWVRQAQKGLEWAVNVSGBGHY 60
OY	61 ADSVKGRPTSSDSKXTAYIQMNSLAEDTAVYYCTA---SGTFPAWGQGLTVTSS 116
DB	61 ADVNGRPTISRNDKXTLYIMNMSLRPEDTAVYCARIRDTPAFHMGQGLTVTSS 119
RESULT 4	
ID	HV32_MOUSE STANDARD; PRT; 115 AA.
AC	P01801;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DE	10-OCT-2003 (Rel. 42, Last annotation update)
DT	Ig heavy chain V-II region J606.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=82099361; Pubmed=6798111;
RA	Johnson N., Slankard J., Paul L.;
RT	"The complete V domain amino acid sequences of two myeloma immu-
RT	noglobulin proteins."
RL	J. Immunol. 128:302-307(1982).
CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS INULIN.
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR	PIR; C92811; AVMS06.
DR	HSSP; P01789; IMCP.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig_1.
DR	SMART; SMO0406; IGv; 1.
DR	PROSITE; PS50835; IG LIKE; 1.
KW	Immunoglobulin V region.
FT	DOMAIN 1 114
FT	DISTUFD 22 98 IG-LIKE BY SIMILARITY.

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FT  NON TER      115      115
SQ  SEQUENCE      115 AA; 12810 MM; B67AD6638A121ASF CRC64;

Query Match
Best Local Similarity 66.9%; Score 412.5; DB 1; Length 115;
Matches 80; Conservative 16; Mismatches 17; Indels 5; Gaps 2;

QY  1 EVOLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWVROAPGKGLIEWVARIDPANDN--T 58
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  1 EVKLSESGGGGLVPGGSLRLSCAASGFTFSPNYMMWRQSEKGLIEWVAIRLSNNYAT 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY  59 IYADVKGRTISSDDSKNTAYLQNNSLRAEDTAVYYCTASGYWFAWGQGLTVTVSS 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  61 HYAESVAGRTFTISDDSKSSVYLQNNLRAEDTGIYCTTG---FAWGGQGLTVTVSA 115
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
HV3H HUMAN      STANDARD;      PRT;      114 AA.
ID  HV3H HUMAN
AC  P01763;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Ig heavy chain V-II region WEA.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC  NCBI_TaxID=9606;
RN  [1]
RP  MEDLINE=83273707; PubMed=6410398;
RX  Gonfi F., Frangione B.;
RT  "Amino acid sequence of the Fv region of a human monoclonal IGM
    (protein WEA) with antibody activity against 3,4-pyruvylated
    galactose in Klebsiella polysaccharides K30 and K33.";
RL  Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983)
CC  -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
    AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
    WALDENSTROM'S MACROGLOBULINEMIA.
CC  -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR  HSP; P01772; 2PB4.
DR  GO: GO:0005576; C:extracellular; NAS.
DR  GO: GO:0003823; P:antigen binding; NAS.
DR  GO: GO:0006955; P:immune response; NAS.
DR  InterPro: IPR003596; Ig_V.
DR  Pfam: PF00047; Ig_1.
DR  SMART: SM00406; IgV_1.
DR  PROSITE: PSS0835; IG_LIKE; 1.
KW  Immunoglobulin V region; Fyrtolidone carboxylic acid.
FT  DOMAIN 1 112 IG-LIKE.
FT  MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT  NON TER 114 114
SQ  SEQUENCE 114 AA; 12256 MM; D88234F8418A07B7 CRC64;

Query Match
Best Local Similarity 66.8%; Score 411; DB 1; Length 114;
Matches 81; Conservative 13; Mismatches 20; Indels 2; Gaps 2;

QY  1 EVOLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWVROAPGKGLIEWVARIDPANDNTIY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  1 QVQLVDSGGGLVPGGSLRLSCASGFTFSPNDMMWRQAPGKGLIEWLSPFGSGGRTIY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY  61 ADVSKGRFTISSDDSKNTAYLQNNSLRAEDTAVYYCTASGYWFAWGQGLTVTVSS 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  61 ADVSKGRFTISRNBSKSLYLQNNSLRAEDTAVYYC-ARQ-WLNMWGGGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
HV3H HUMAN      STANDARD;      PRT;      116 AA.
ID  HV3H HUMAN
AC  P01761;

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DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Ig heavy chain V-II region GHL.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC  NCBI_TaxID=9606;
RN  [1]
RP  MEDLINE=75059123; PubMed=4803843;
RX  Watanabe S., Barnikol H.U., Horn J., Berttram J., Hilschmann N.;
RT  "The primary structure of a monoclonal IGM-immunoglobulin
    (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
    type), subgroup H III. Architecture of the complete IGM-molecule.";
RL  Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN  [2]
RP  REVISION TO 28-33.
RA  Hilschmann N.;
RL  Submitted (JUN-1975) to the PIR data bank.
CC  -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
    MACROGLOBULIN.
CC  -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR  HSP; A02064; M3HUGL.
DR  GO: GO:0005576; C:extracellular; NAS.
DR  GO: GO:0003823; P:antigen binding; NAS.
DR  GO: GO:0006955; P:immune response; NAS.
DR  InterPro: IPR007110; Ig_V.
DR  InterPro: IPR003596; Ig_V.
DR  Pfam: PF00047; Ig_1.
DR  SMART: SM00406; IgV_1.
DR  PROSITE: PSS0835; IG_LIKE; 1.
KW  Immunoglobulin V region.
FT  DOMAIN 1 112 IG-LIKE.
FT  NON TER 116 116
SQ  SEQUENCE 116 AA; 12730 MM; 2C67CA9A9AAA1282 CRC64;

Query Match
Best Local Similarity 65.8%; Score 406; DB 1; Length 116;
Matches 80; Conservative 8; Mismatches 28; Indels 0; Gaps 0;

QY  1 EVOLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWVROAPGKGLIEWVARIDPANDNTIY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  1 EVOLVESGGDLVPGGSLRLSCASGFBFBELGHTWRQAPGKGLIEWANIKZSGSZBY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY  61 ADVSKGRFTISSDDSKNTAYLQNNSLRAEDTAVYYCTASGYWFAWGQGLTVTVSS 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  61 VDSVKGRTISRDVAKSKSLYLQNNSLRAEDTALYYCARGWGGGQGLTVTVST 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
HV3H HUMAN      STANDARD;      PRT;      122 AA.
ID  HV3H HUMAN
AC  P01769;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Ig heavy chain V-II region GA.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC  NCBI_TaxID=9606;
RN  [1]
RP  MEDLINE=74175307; PubMed=4208843;
RX  Florent G., Lehman D., Putnam F.W.;
RT  "The switch point in mu heavy chains of human IGM immunoglobulins.";
RL  Biochemistry 13:2482-2498(1974).
CC  -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
    MACROGLOBULIN.
CC  -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR  PIR; A02052; M3HUGA.

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DR HSSP; P01772; 2PB4.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; F:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR Immunoglobulin V region; Fyrtolidene carboxylic acid.  
 KW DOMAIN 1 112  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT NON TER 122 122  
 FT TER 122 122  
 SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;

Query Match 65.8%; Score 406; DB 1; Length 122;  
 Best Local Similarity 61.5%; Pred. No. 5.3e-35;  
 Matches 75; Conservative 18; Mismatches 23; Indels 6; Gaps 1;

QY 1 EVOLVESGGGLVOPGGSLRLSCAASGFTFNKIDTYIHVWVROAPGKLEWVA--RIDPANDNTY 60  
 DB 1 QVZLVZSGGAVZPRSRSLRLSCAASGFTFTYAMHWVQAQKGLZMLSVISYGBEZY 60  
 QY 61 ADSVKGRTTSSDSSKNTAYLQNNSLRAEDTAVVYCTASGYWFA-----YMGQGLTVT 114  
 DB 61 AASVKGRTTISRBSKNTMYLQNNSLRAEDTAVVYCTASGYWFA-----YMGQGLTVT 120  
 QY 115 SS 116  
 DB 121 SS 122

RESULT 8  
 HV27\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01756; 2PB4.  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region AA.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=78158406; PubMed=417344;  
 RA Vrana M., Rudikoff S., Potter M.;  
 RT "Sequence variation among heavy chains from inulin-binding myeloma  
 RT proteins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961 (1978).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 CC BINDS INULIN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A93818; AVMSAB.  
 DR HSSP; P01810; 2PB4.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 >113  
 FT DISULFID 22 98  
 FT NON TER 113 113  
 FT TER 113 113  
 SQ SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;

Query Match 65.7%; Score 405.5; DB 1; Length 113;  
 Best Local Similarity 68.1%; Pred. No. 5.5e-35;  
 Matches 79; Conservative 14; Mismatches 18; Indels 5; Gaps 2;

QY 1 EVOLVESGGGLVOPGGSLRLSCAASGFTFNKIDTYIHVWVROAPGKLEWVA--RIDPANDNT 58  
 DB 1 EVLLESGGGLVOPGGSMRLSCAASGFTFTSNYMMNWVROSPKGLWVAEIRLKSHTYAT 60

DB 1 EVLLESGGGLVOPGGSMRLSCAASGFTFTSNYMMNWVROSPKGLWVAEIRLKSHTYAT 60  
 QY 59 IYADSVKGRFTTSSDSSKNTAYLQNNSLRAEDTAVVYCTASGYWFAWGGGLTVT 114  
 DB 61 HYAESVKGRTTISRBSKNTMYLQNNSLRAEDTAVVYCTASGYWFAWGGGLTVT 113

RESULT 9  
 HV30\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01799;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region ABE-47N.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=77134726; PubMed=402936;  
 RA Vrana M., Rudikoff S., Potter M.;  
 RT "Heavy-chain variable-region sequence from an inulin-binding myeloma  
 RT protein.";  
 RL Biochemistry 16:1170-1175 (1977).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 CC BINDS INULIN.  
 DR PIR; A90400; AVMSB7.  
 DR HSSP; P01810; 2PB4.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 >113  
 FT DISULFID 22 98  
 FT NON TER 113 113  
 FT TER 113 113  
 SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;

Query Match 65.7%; Score 405.5; DB 1; Length 113;  
 Best Local Similarity 68.1%; Pred. No. 5.5e-35;  
 Matches 79; Conservative 15; Mismatches 17; Indels 5; Gaps 2;

QY 1 EVOLVESGGGLVOPGGSLRLSCAASGFTFNKIDTYIHVWVROAPGKLEWVA--RIDPANDNT 58  
 DB 1 EVLLESGGGLVOPGGSMRLSCAASGFTFTSNYMMNWVROSPKGLWVAEIRLKSHTYAT 60  
 QY 59 IYADSVKGRFTTSSDSSKNTAYLQNNSLRAEDTAVVYCTASGYWFAWGGGLTVT 114  
 DB 61 HYAESVKGRTTISRBSKNTMYLQNNSLRAEDTAVVYCTASGYWFAWGGGLTVT 113

RESULT 10  
 HV31\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01800;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region T957.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=81216632; PubMed=6787122;  
 RA Rudikoff S., Potter M.;  
 RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:  
 RT evidence for a new heavy chain joining segment.";

	J.	Miscellaneous:	This chain was isolated from a myeloma protein that binds insulin.
CC	-I-	Similarity:	Contains 1 immunoglobulin-like domain.
CC	PIR,	A92810;	AWMS57.
DR	HSSP,	P01810;	2FBJ.
DR	InterPro,	IIPR007110;	Ig-Like.
DR	InterPro,	IIPR003596;	Ig_v.
DR	Fam;	PF00047;	Ig; 1.
DR	SMART;	SMD0406;	IGV; 1.
DR	PROSITE;	PS50835;	IG LIKE; 1.
KW	Immunoglobulin V region.	>113	IG-LIKE.
FT	DISEUPTD	22	98 BY SIMILARITY.
FT	NON TER	113	
SO	SEQUENCE	113 AA;	12732 MW; 26618P626B59859E CRC64;
	Query Match	Best Local Similarity	65.6%; Score 404.5; DB 1; Length 113;
	Matches	79; Conservative	13; Mismatches 19; Indels 5; Gaps 2
Qy	1	EVLVESGGGVLPQGSGLRSLCAAGFNIIKDTYIHVMVRQAPEKGLEWVA--RIDPDANDNT	58
Db	1	EVKLEESGGLIVPGEGSKMLCSVASGFPPSNMNMVVNGSPKGLEWAERLKSHNET	60
Qy	59	IYADSVKGRFTISDDSTCKTAYLQNNSIRAEEDTAIVYYCTASGYPMFYWGQTLTVV	114
Db	61	HYASVSFKRFRTISRDSKSSVYLQNNIIRAEDTGICYCTTG---PAYMGQTLLTVV	113
	RESULT 11		
ID	HVO1_RAT	STANDARD;	PRT; 142 AA.
AC	P01805;		
DT	21-JUL-1986	(Rel. 01, Created)	
DT	21-JUL-1986	(Rel. 01, Last sequence update)	
DT	10-OCT-2003	(Rel. 42, Last annotation update)	
OS	Ig heavy chain V region IR2 precursor.		
DE	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxId=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=83064537; PubMed=6292865;		
RA	Hellman L., Petersson U., Engstrom A.; Karlsson T., Benrich H.;		
RT	"Structure and evolution of the heavy chain from rat immunoglobulin		
RL	Nucleic Acids Res. 10:6041-6049(1982)." ;		
CC	-I- MISCELLANEOUS: THE MRNA WAS ISOLATED FROM AN IGE-SECRETING IMMUNOBLASTOMA THAT ARISES SPONTANEOUSLY IN LOU/C/WEL RATS.		
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.		
DR	PIR; A02075; EVTRR2.		
DR	HSSP; P01789; IMCP.		
DR	InterPro; IPR007110;	Ig-Like.	
DR	InterPro; IPR003596;	Ig_v.	
DR	Ffam; PF00047;	Ig; 1.	
DR	SMART; SMD0406;	IGV; 1.	
DR	PROSITE; PS50835;	IG LIKE; 1.	
DR	Immunoglobulin V region; Signal.		
FT	SIGNAL	1	19
FT	CHAIN	20	142 IG HEAVY CHAIN V REGION IR2.
FT	DOMAIN	20	133 IG-LIKE.
FT	NON TER	142	142
SO	SEQUENCE	142 AA;	DE29BCFE745DF3B CRC64;
	Query Match	Best Local Similarity	65.2%; Score 402.5; DB 1; Length 142;
	Matches	78; Conservative	15; Mismatches 23; Indels 7; Gaps 3
Qy	1	EVLVESGGGVLPQGSGLRLSCAAGFNIIKDTYIHVMVRQAPEKGLEWVARIDPDANDNT	59
Db	20	EVKLEESGGLIVPGEMSYVLCSGTSGTFESDYMMWMVROAPEKGLEWVAERLNKNNTYA	79

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QY      60  -YADSVKSGFETISDDSKNTATVLONNSLRADETAVYCYLA--SGY---WPAWYGQGLVLT 113
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      80  YKSKSLKGFPLTSRDSDSKSVYLVLONNIRSEDTGIYICSGYGVISENPFVYWGQGLVLT 139
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      114 VSS 116
      |||
DB      140 VSS 142

RESULT 12
HV33 MOUSE STANDARD; PRT; 115 AA.
ID HV33 MOUSE
AC P01802;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1g heavy chain V-II region W3082.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
[1]
RN
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N, Slankard J, Paul L, Hood L;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins."
RL J. Immunol. 128:302-307(1982).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
PRR; D92811; AVM82.
DR HSBP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR Immunoglobulin V region.
KM DOMAIN 1 114 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12887 MW; 984517648C121C5A CRC64;

Query Match 65.1%; Score 401.5; DB 1; Length 115;
Best Local Similarity 66.1%; Pred. No. 1.5e-34;
Matches 78; Conservative 16; Mismatches 19; Indels 5; Gaps 2

QY      1 EVOLVSGGGLVOPGGSLRLSCAAGFNIKDTYIHWVQAQPGKLEWYA--RIDPANDNT 58
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      1 EVLLEESGGGLVOPGGSKMLSCVAGCFPSNYMMWVQSEPKLEWVAEIRLSHRYAT 60

QY      59 IVADSVKGFETISDDSKNTATVLONNSLRADETAVYCYCTASGYWPAWYGQGLVTVSS 116
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      61 HVASVKGKGFETISRDSDSKSVYLVLONNIRPEDTGIYCYCTG---FAWVGQGLVTVSSA 115

RESULT 13
HV16 MOUSE STANDARD; PRT; 136 AA.
ID HV16 MOUSE
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1g heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
[1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;

```

RA Bothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "heavy chain variable region contribution to the NPb family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region."  
 RL Cell 24:625-637(1981).  
 RN [2]  
 RP SEQUENCE OF 17-136.  
 RX MEDLINE=77100366; PubMed=401950;  
 RA Adeybo K., Milstein C., Secher D.S.;  
 RT "Molecular analysis of spontaneous somatic mutants."  
 RL Nature 265:299-304(1977).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; J00522; AAD15290.1; -;  
 DR PIR; B90809; GIMS21.  
 DR PDB; 1IGC; 03-JUN-95.  
 DR InterPro; IPR007110; Ig\_1ike.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin V region; Signal; 3D-structure.  
 FT NON\_TER 1  
 FT SIGNAL 16  
 FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.  
 FT DOMAIN 115 119 D SEGMENT.  
 FT DOMAIN 120 136 JH4 SEGMENT.  
 FT DISULFID 38 112  
 FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).  
 FT CONFLICT 89 90 DN -> ND (IN REF. 2).  
 FT CONFLICT 115 115 W -> H (IN REF. 2).  
 FT CONFLICT 120 120 Y -> W (IN REF. 2).  
 FT NON\_TER 136  
 SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDEF7016 CRC64;  
 Query Match 64.7%; Score 401; DB 1; Length 136;  
 Best Local Similarity 66.7%; Pred. No. 2e-34;  
 Matches 80; Conservative 9; Mismatches 27; Indels 4; Gaps 1;  
 QY 1 EVOLVESGGGLVPGGSLRLSQAAGFENIKDTYTHVWRQAPGKLEWVA--RIDPANDNT 60  
 DB 17 DVLVESGGGLVPGGSLRLSCAASGFTFSFGMHWRQAPGKLEWVA--YISSGSLHY 76  
 QY 61 ADSYKGRFTISSDSKNTAYLQNMNLRAPEDTAVYCTASG----YFAYNGGGLVTV 116  
 DB 77 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDYAMTCARWGYPPYANDYWGQGVTVSS 136  
 RESULT 14  
 HV28 MOUSE STANDARD; PRT; 113 AA.  
 ID HV28 MOUSE  
 AC P01797;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-III region U61.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76158406; PubMed=417344;  
 RA Virena M., Rudikoff S., Potter M.;  
 RT "Sequence variation among heavy chains from inulin-binding myeloma  
 RT proteins."

RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 CC BINDS INULIN  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; B93818; AVM561.  
 DR HSSP; P01810; 2FBJ.  
 DR InterPro; IPR007110; Ig\_1ike.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin V region.  
 FT DOMAIN 1 >113 IG-LIKE.  
 FT DISULFID 22 98 BY SIMILARITY.  
 FT NON\_TER 113 113  
 SQ SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;  
 Query Match 64.7%; Score 399.5; DB 1; Length 113;  
 Best Local Similarity 67.2%; Pred. No. 2.3e-34;  
 Matches 78; Conservative 14; Mismatches 19; Indels 5; Gaps 2;  
 QY 1 EVOLVESGGGLVPGGSLRLSQAAGFENIKDTYTHVWRQAPGKLEWVA--RIDPANDNT 58  
 DB 1 EVKLEESGGGLVPGGSMKLSCAASGFTFSNGYMWNRQSPKGLWVAEIRKSHNYAT 60  
 QY 59 IYADSVKGRFTISSDSKNTAYLQNMNLRAPEDTAVYCTASGWFAYNGGGLVTV 114  
 DB 61 HYAESYKGRFTISRDSKSVYLQNMNLRAPEDTGIYCTTG--FAYWGGLTVPV 113  
 RESULT 15  
 HV3U HUMAN STANDARD; PRT; 120 AA.  
 ID HV3U HUMAN  
 AC P01782;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-III region DOB.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=80020921; PubMed=114209;  
 RA Steiner L.A., Garcia Pardo A., Margolies M.N.;  
 RT "Amino acid sequence of the heavy-chain variable region of the  
 RT crystallizable human myeloma protein Dob.";  
 RL Biochemistry 18:4068-4080(1979).  
 RN [2]  
 RP CRYSTALLIZATION.  
 RX MEDLINE=80020920; PubMed=114208;  
 RA Steiner L.A., Lopes A.D.;  
 RT "The crystallizable human myeloma protein Dob has a hinge-region  
 RT deletion.";  
 RL Biochemistry 18:4054-4067(1979).  
 CC -1- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE  
 CC HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN  
 CC DISULFIDE BONDS.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A90431; GHJUD.  
 DR HSSP; P01772; 2FBJ.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig\_1ike.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin V region.  
 FT DOMAIN 1 112 IG-LIKE.  
 FT NON\_TER 120 120

SQ SEQUENCE 120 AA; 13440 MW; 880DDE307C4B2627 CRC64;

Query Match 64.5%; Score 398; DB 1; Length 120;

Best Local Similarity 66.1%; Pred. No. 3.5e-34;

Matches 80; Conservative 10; Mismatches 25; Indels 6; Gaps 2;

QY 1 EVQLVESGGGLVOPGSGLRISCAASGFNIDKTYIHWRQAPGKGLEWVARIDPANDNTIY 60

Db 1 EVQLVESGGGLVOPGSGLRISCAASGFNIDKTYIHWRQAPGKGLEWVARIDPANDNTIY 60

QY 61 ADSVKGRFTISSDSDSKNTATLQANSLPAEDTAVYYCTASG-----WFAWGGTILYTVS 115

Db 61 ADSVKGRFAISRDNQAQKTLYLQILIRPEDTAFYYC-AKGYIWNQNWPFDSWGCGTILYTVS 119

QY 116 S 116

Db 120 S 120

Search completed: May 13, 2004, 16:57:24

Job time : 23.7857 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: May 13, 2004, 16:56:47 ; Search time 37.125 Seconds

(without alignments)  
279,830 Million cell updates/sec

Title: A1 US-09-910-483-7

Perfect score: 566  
Sequence: 1 D1QMTQSPSSLSASVGRVT.....QQSNMPTFGQGTKEIKR 108Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.78:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	490	86.6	127	2	S40367	Ig kappa chain V-J
2	483	85.3	123	2	S40331	Ig kappa chain - h
3	482	85.2	108	2	B49047	Ig kappa chain V r
4	480	84.8	129	2	S40369	Ig kappa chain - h
5	479	84.6	125	2	S40333	Ig kappa chain V-J
6	474	83.7	108	2	S19674	Ig kappa chain V r
7	471	83.2	108	2	S44122	Ig kappa chain V r
8	470	83.0	125	2	S40349	Ig kappa chain V-J
9	469	82.9	117	2	S46371	Ig kappa chain V-J
10	468	82.7	122	2	S40370	Ig kappa chain - h
11	465	82.2	108	1	K1HUBN	Ig kappa chain V-I
12	464	82.0	109	2	S31998	Ig kappa chain - h
13	463	81.8	107	2	S36269	Ig kappa chain V
14	463	81.8	108	1	K1HUBU	Ig kappa chain V-I
15	463	81.8	120	2	S46370	Ig kappa chain V-J
16	463	81.8	123	2	S40313	Ig kappa chain V-J
17	462	81.6	125	2	S40353	Ig kappa chain V-J
18	462	81.6	131	2	S40352	Ig kappa chain V-J
19	461	81.4	108	1	K1HUBU	Ig kappa chain V-I
20	461	81.4	117	2	S46376	Ig kappa chain V-J
21	461	81.4	125	2	S40316	Ig kappa chain - h
22	460	81.3	108	1	K1HUBU	Ig kappa chain V-I
23	460	81.3	108	2	S47182	Ig kappa chain V-I
24	459.5	81.2	124	2	S40336	Ig kappa chain V-J
25	459	81.1	107	2	S36262	Ig kappa chain V
26	459	81.1	109	2	S31981	Ig kappa chain - h
27	459	81.1	132	2	S40334	Ig kappa chain - h
28	458.5	81.0	125	2	S40315	Ig kappa chain - h
29	458	80.9	107	2	S36264	Ig kappa chain V

30	458	80.9	108	1	K1HUBE	Ig kappa chain V-I
31	457	80.7	129	1	K1HUMK	Ig kappa chain pre
32	456	80.6	129	2	S40317	Ig kappa chain - h
33	455	80.4	126	2	S40335	Ig kappa chain V-J
34	454.5	80.3	107	2	S36275	Ig kappa chain V
35	452	79.9	122	2	S40314	Ig kappa chain - h
36	452	79.9	129	2	S52793	Ig kappa chain V r
37	450	79.5	107	2	JL0139	Ig kappa chain V r
38	450	79.5	108	1	K1HUBU	Ig kappa chain V-I
39	450	79.5	108	2	S36279	Ig kappa chain V
40	450	79.5	129	2	S52792	Ig kappa chain V r
41	449.5	79.4	106	2	PC2397	anti-tetanus toxin
42	449	79.3	130	2	S40368	Ig kappa chain - h
43	448	79.2	108	1	K1HUBE	Ig kappa chain V-I
44	447	79.0	125	2	S40350	Ig kappa chain - h
45	447	79.0	128	2	S46372	Ig kappa chain var

## ALIGNMENTS

## RESULT 1

S40367  
Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40367

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40367

A&gt;Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-127 &lt;KLE&gt;

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:33-107/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 86.6%; Score 490; DB 2; Length 127;  
Best Local Similarity 89.8%; Pred. No. 9,7e-34;  
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy	1	D1QMTQSPSSLSASVGRVTTTCRASQISNNLHWYQKRGKAPKLIYASQISGVPS	60
Db	18	D1QMTQSPSSLSASVGRVITCRASQISNNLHWYQKRGKAPKLIYASQISGVPS	77
Qy	61	RFSGSGSGTDFTLTISLSLOPEDPATYCCQSNMPTFGQGTKEIKR	108
Db	78	RFSGSGSGTDFTLTISLSLOPEDPATYCCQSNMPTFGQGTKEIKR	125

## RESULT 2

S40331  
Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40331

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40331

A&gt;Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-123 &lt;KLE&gt;

A:Cross-references: EMBL:X72441; NID:G441350; PIDN:CA51109.1; PID:G441351

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:32-106/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 85.3%; Score 483; DB 2; Length 123;



submitted to the EMBL Data Library, March 1994

A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r

A:Reference number: S44105

A:Accession: S44122

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-108 <HAM>

A:Cross-references: EMBL:Z31390; NID:9472976; PIDN:CAA83265.1; PID:940533

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 471; DB 2; Length 108;

Best Local Similarity 88.0%; Pred. No. 3.1e-32;

Matches 95; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGVGRVITTCRASQSIISNNLHWYQOKPKAPKLLIYHASQISGVPS 60

DB 1 DIQMTQSPSSLSASVGVGRVITTCRASQSIISNNLHWYQOKPKAPKLLIYHASQISGVPS 60

QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMWPYFGQGTKEIKR 108

DB 61 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMWPYFGQGTKEIKR 108

#### RESULT 8

S40349

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000

C:Accession: S40349

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Status: Preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLE>

A:Cross-references: EMBL:X72459; NID:9441386; PIDN:CAA51127.1; PID:9441387

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 470; DB 2; Length 125;

Best Local Similarity 86.9%; Pred. No. 4.2e-32;

Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 IOMTQSPSSLSASVGVGRVITTCRASQSIISNNLHWYQOKPKAPKLLIYHASQISGVPSR 61

DB 19 IOMTQSPSSLSASVGVGRVITTCRASQSIISNNLHWYQOKPKAPKLLIYHASQISGVPSR 78

QY 62 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMWPYFGQGTKEIKR 108

DB 79 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMWPYFGQGTKEIKR 125

#### RESULT 9

S46371

Ig kappa chain V-J region (T24-3) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 27-Jan-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000

C:Accession: S46371; S38645

R:Bensimon, C.; Chastagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene reas

A:Reference number: S46369; MUID:94313975; PMID:8039491

A:Accession: S46371

A:Molecule type: mRNA

A:Residues: 1-117 <BEN>

A:Cross-references: EMBL:Z27172; NID:9415959; PIDN:CAA81696.1; PID:9415960

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:23-97/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 469; DB 2; Length 117;

Best Local Similarity 85.5%; Pred. No. 4.8e-32;

Matches 94; Conservative 6; Mismatches 8; Indels 2; Gaps 1;

QY 1 DIQMTQSPSSLSASVGVGRVITTCRASQSIISNNLHWYQOKPKAPKLLIYHASQISGVPS 60

DB 8 DIQMTQSPSSLSASVGVGRVITTCRASQSIISNNLHWYQOKPKAPKLLIYHASQISGVPS 67

QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMWPYFGQGTKEIKR 108

DB 68 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMWPYFGQGTKEIKR 117

#### RESULT 10

S40370

Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40370

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40370

A:Status: Preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-122 <KLE>

A:Cross-references: EMBL:X72480; NID:9441428; PIDN:CAA51148.1; PID:9441429

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 82.7%; Score 468; DB 2; Length 122;

Best Local Similarity 87.0%; Pred. No. 6.1e-32;

Matches 94; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGVGRVITTCRASQSIISNNLHWYQOKPKAPKLLIYHASQISGVPS 60

DB 15 DIQMTQSPSSLSASVGVGRVITTCRASQSIISNNLHWYQOKPKAPKLLIYHASQISGVPS 74

QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMWPYFGQGTKEIKR 108

DB 75 RFSGSGSGTDFTLTISLQPEDPATYCCQSNMWPYFGQGTKEIKR 122

#### RESULT 11

K1HUBN

Ig kappa chain V-I region (Ban) - human

C:Species: Homo sapiens (man)

C:Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 15-Aug-1997

C:Accession: A01878

R:Dwulet, F.E.; O'Connor, T.P.; Benson, M.D.

Mol. Immunol. 23, 73-78, 1986

A:Title: Polymorphism in a kappa I primary (AI) amyloid protein (BAN).

A:Reference number: A01878; MUID:86174817; PMID:3083240

A:Accession: A01878

A:Molecule type: protein

A:Residues: 1-108 <DWU>

C:Genetics:

A:Gene: GDB:IGKVL

A:Cross-references: GDB:136264

A:Map position: 2p12-2p12

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la;

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: amyloid; heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>

F:24-34/Region: complementarity-determining 1

F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3  
F:89-97/Region: complementarity-determining 3  
F:98-107/Region: framework 4  
F:23-88/Disulfide bonds: #status predicted

Query Match 82.2%; Score 465; DB 1; Length 108;  
Best Local Similarity 83.3%; Pred. No. 9.5e-32;  
Matches 90; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTITCRASQSSINNLHWQKRGKAPKLLIYHASQISGVPS 60  
DQ 1 DIQLTQSPSSLSASVGDRTITCRASQSSINNLHWQKRGKAPKLLIYDASTLQSGVPS 60

QY 61 RFGSGSGTDFLTITSLQPEDFATYYCOQSNMWPYTFGQGTVEIKR 108  
DQ 61 NFGSGSGTDFLTITSLQPEDFATYYCOQSNMWPYTFGQGTVEIKR 108

## RESULT 12

S31998  
Ig kappa chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000

C/Accession: S31998

R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.

Submitted to the EMBL Data Library, June 1992

A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as

A/Reference number: S31977

A/Accession: S31998

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-109 <PCR>

C/Cross-references: EMBL:Z15081; NID:G38501; PIDN:CAA78790.1; PID:G38502

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 464; DB 2; Length 109;  
Best Local Similarity 85.2%; Pred. No. 1.2e-31;  
Matches 92; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTITCRASQSSINNLHWQKRGKAPKLLIYHASQISGVPS 60  
DQ 1 ELVMTQSPSSLSASVGDRTITCRASQSSINNLHWQKRGKAPKLLIYASSTLQSGVPS 60

QY 61 RFGSGSGTDFLTITSLQPEDFATYYCOQSNMWPYTFGQGTVEIKR 108  
DQ 61 RFGSGSGTDFLTITSLQPEDFATYYCOQSNMWPYTFGQGTVEIKR 108

## RESULT 13

S36269  
Ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000

C/Accession: S36269

R/Gilfiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A/Title: Human anti-self antibodies with high specificity from phage display libraries.

A/Reference number: S36266; MUID:93178448; PMID:7679990

A/Accession: S36269

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-107 <GDI>

A/Cross-references: EMBL:Z18838; NID:G33422; PIDN:CAA79290.1; PID:G939915

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 463; DB 2; Length 107;  
Best Local Similarity 85.0%; Pred. No. 1.4e-31;  
Matches 91; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTITCRASQSSINNLHWQKRGKAPKLLIYHASQISGVPS 60  
DQ 1 DIOMTQSPSSLSASVGDRTITCRASQSSINNLHWQKRGKAPKLLIYGTSLQSGVPS 60

QY 61 RFGSGSGTDFLTITSLQPEDFATYYCOQSNMWPYTFGQGTVEIKR 107  
DQ 61 RFGSGSGTDFLTITSLQPEDFATYYCOQSNMWPYTFGQGTVEIKR 107

## RESULT 14

K1H0HU  
Ig kappa chain V-I region (Hau) - human

C/Species: Homo sapiens (man)

C/Date: 24-Apr-1984 #sequence\_revision 02-Jul-1998 #text\_change 21-Jan-2000

C/Accession: A01868; S02574

R/Matnabe, S.; Hillebrand, N.

Hoppe-Seyler's Z. Physiol. Chem. 351, 1291-1295, 1970

A/Title: The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subg

A/Reference number: A01868; MUID:71032830; PMID:4097974

A/Accession: A01868

A/Molecule type: protein

A/Residues: 1-108 <WAT>

A/Note: The C region of this chain has the Inv (3) marker

R/Steiner, V.; Chang, J.Y.

FEBS Lett. 222, 6-10, 1987

A/Title: Chemical modification of the carboxyl groups of protein substrates enhances the

A/Reference number: S02572; MUID:88005152; PMID:3115831

A/Contents: annotation

C/Comment: This is a Bence Jones protein.

C/Genetics:

A/Gene: GDB:IGKV1

A/Cross-references: GDB:136264

A/Map position: 2p12-2p12

C/Complex: an immunoglobulin heterotrimer subunit consists of two identical light (kappa)

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 463; DB 1; Length 108;  
Best Local Similarity 85.2%; Pred. No. 1.4e-31;  
Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTITCRASQSSINNLHWQKRGKAPKLLIYHASQISGVPS 60  
DQ 1 DIOMTQSPSSLSASVGDRTITCRASQSSINNLHWQKRGKAPKLLIYASSTLQSGVPS 60

QY 61 RFGSGSGTDFLTITSLQPEDFATYYCOQSNMWPYTFGQGTVEIKR 108  
DQ 61 RFGSGSGTDFLTITSLQPEDFATYYCOQSNMWPYTFGQGTVEIKR 108

## RESULT 15

S46370  
Ig kappa chain V-J region (T23-9) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 27-Jan-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000

C/Accession: S46370; S38644

R/Beniston, C.; Chastagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene reat

A/Reference number: S46369; MUID:94313975; PMID:8034991

A/Accession: S46370

A/Molecule type: mRNA

A/Residues: 1-120 <BEN>

A/Cross-references: EMBL:Z27171; NID:G415957; PIDN:CAA01695.1; PID:G415958

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 463; DB 2; Length 120;  
Best Local Similarity 85.5%; Pred. No. 1.5e-31;

Matches 94; Conservative 6; Mismatches 8; Indels 2; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDNRVTITCRASQISNNLHWQOKPKAKLITYHASQISGVPS 60  
 |||||  
 Db 11 DIQMTQSPSSLSASVGDNRVTITCRASRISSEFLNMYQOKPKAPOLLITYAVSRLOSGVPS 70  
 |||||

QY 61 RFGSGSGGTDFLLTISLQPEDFATYYCOQSNWSP--YTFGQGTKEIKR 108  
 |||||  
 Db 71 RFGSGSGGTDFLLTISLQPEDFATYYCOQSFNPPETTFGQGTKEIKR 120  
 |||||

Search completed: May 13, 2004, 17:03:14  
 Job time : 38.125 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 16:56:47 ; Search time 39.875 Seconds

(without alignments)  
279.830 Million cell updates/sec

Title: US-09-910-483-5

Perfect score: 617  
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....TASGYWFAWGQGLTVTVSS 116

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*

1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	458.5	74.3	119	2	S31107 Ig heavy chain - h
2	452.5	73.3	117	2	S31109 Ig heavy chain - h
3	452.5	73.3	119	2	C36005 Ig heavy chain V r
4	451.5	73.2	140	2	S31588 Ig heavy chain V r
5	450.5	73.0	121	2	S19666 Ig heavy chain V r
6	448	72.6	120	2	S48798 Ig heavy chain V r
7	447.5	72.5	138	2	S31666 Ig heavy chain V r
8	446.5	72.4	119	2	D36005 Ig heavy chain V r
9	446.5	72.4	143	2	S23624 Ig heavy chain V r
10	446	72.3	140	2	S70442 Ig heavy chain pre
11	445.5	72.2	123	2	S31114 Ig heavy chain - h
12	445	72.1	114	2	S31120 Ig heavy chain - h
13	445	72.1	114	2	S46350 Ig heavy chain V r
14	444.5	72.0	125	2	S30531 Ig heavy chain V r
15	444	72.0	128	2	S44111 Ig heavy chain V-D
16	444	72.0	128	2	S26786 Ig heavy chain V r
17	443.5	71.9	135	2	S31598 Ig heavy chain V r
18	442	71.6	124	2	S20782 Ig heavy chain V r
19	441.5	71.6	132	2	S31603 Ig heavy chain V r
20	438.5	71.1	119	2	S31108 Ig heavy chain - h
21	438	71.0	139	2	PC1213 Ig heavy chain pre
22	437.5	70.9	140	2	S31686 Ig heavy chain V r
23	436.5	70.7	127	2	S38489 Ig heavy chain - h
24	436	70.7	139	2	S31674 Ig heavy chain V r
25	436	70.7	147	2	I37780 Ig variable region
26	435.5	70.6	120	2	S36273 Ig heavy chain V r
27	435.5	70.6	121	2	G36005 Ig heavy chain V r
28	435	70.5	128	2	S26790 Ig heavy chain V r
29	434.5	70.4	121	2	S26798 Ig heavy chain V r

30	434.5	70.4	121	2	I55673 Ig heavy chain - h
31	434	70.3	122	2	S31117 Ig heavy chain - h
32	433.5	70.3	120	2	S36278 Ig heavy chain V r
33	433.5	70.3	130	2	S31601 Ig heavy chain V r
34	433	70.2	116	2	S31110 Ig heavy chain - h
35	433	70.2	128	2	S48797 Ig heavy chain V r
36	432	70.0	118	2	S31116 Ig heavy chain - h
37	431.5	69.9	121	2	S31104 Ig heavy chain (su
38	431.5	69.9	123	2	A36006 Ig heavy chain V r
39	431	69.9	120	2	S31112 Ig heavy chain - h
40	431	69.9	122	2	S31679 Ig heavy chain V r
41	430.5	69.8	134	2	S31679 Ig heavy chain V r
42	430	69.7	122	2	S20772 Ig heavy chain V r
43	428.5	69.4	117	2	S78486 Ig heavy chain V r
44	428	69.4	122	2	S30533 Ig heavy chain V r
45	427.5	69.3	121	2	H36005 Ig heavy chain V r

#### ALIGNMENTS

##### RESULT 1

S31107  
Ig heavy chain - human  
C/Species: Homo sapiens (man)  
C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C/Accession: S31107  
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, Eur. J. Immunol. 22, 247-251, 1992  
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
A/Reference number: S31104; MUID:92111633; PMID:1730252  
A/Accession: S31107  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-119 <RAA>  
A/Cross-references: EMBL:X62955  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.3%; Score 458.5; DB 2; Length 119;  
Best Local Similarity 75.6%; Pred. No. 9.4e-34;  
Matches 90; Conservative 7; Mismatches 19; Indels 3; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFRNIKDTYHWRAQAPGKLEWVARIDPANDITY 60  
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWRQAPGKLEWVAISGSGSTYY 60  
Qy 61 ADSVKGRTTSSDSDKMTAYIQNMSLRAPDAVYYCT---ASGYWFAWGQGLTVTVSS 116  
Db 61 ADSVKGRTTSSDSDKMTAYIQNMSLRAPDAVYYCAKDPGASYFPDYGQGLTVTVSS 119

##### RESULT 2

S31109  
Ig heavy chain - human  
C/Species: Homo sapiens (man)  
C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, Eur. J. Immunol. 22, 247-251, 1992  
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
A/Reference number: S31104; MUID:92111633; PMID:1730252  
A/Accession: S31109  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-117 <RAA>  
A/Cross-references: EMBL:X62960  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-100/Domain: immunoglobulin homology <IMM>

Query Match	73.3%	Score 452.5	DB 2	Length 117
Best Local Similarity	76.3%	Pred. No. 3.1e-33		
Matches 90	Conservative 7	Mismatches 18	Indels 3	Gaps 2

[illegible]

```

RESULT 3
C36005
I: heavy chain V region (30pt) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C:Accession: C36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:211273
A:Accession: C36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: GB:M18513
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMW>

```

Query Match	73.3%	Score 452.5;	DB 2;	Length 119;
Best Local Similarity	74.8%	Pred. No. 3.2e-33;		
Matches	89;	Conservative	6;	Mismatches 21; Indels 3; Gaps
QY	1	EVOLVESGGGLVDPGSGILRLSCAASGFNIKDTYIHWVRAPAGKGLPMVARIPANDNTLY	60	
		:           :   :		
Dd	1	EVLVLSSGGGLVDPGSGILRLSCAASGFTTBSYMSWROAPGKGLPMVAISLSSGSSTYY	60	
		:           :   :		
QY	61	ADSVKGRFTISDDSKNATYLQNNSLRAEEDTAVYYCTASGYW---FAYWGQGTLVTVSS	116	
		:           :   :		
Dd	61	ADSVKGRFTISRDKSNATYLTQNSLRAEEDTAVYYCAAKAGMGSGDYGQGLTVTVSS	119	
		:           :   :		

```

RESULT 4
S31588
IG heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31588
R/Cislnsler, A.M.; Gaucher, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A/Description: The mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31588
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-140 <CUI>
A/Cross-references: EMBL:Z14200, NID:g30957, PIDD:CAA7569.1, PIDT:g30958
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
C/34-117/Domains: immunoglobulin homology <IMM>

```

```

QY      1  EYVLVESGGCGVLPQGGSTRRLSCAASGPRRIKDTYTHYWRQAPGGLGEMWVARIPADNDNTY 60
        20  EYVLVESGGGGLVLPQGGSTRRLSCAASGPRFSSVYASWWRQAPGGLGEMWVARISGSGSTY 79
        Matches 91; Conservative 6; Mismatches 19; Indels 5; Gaps 2
        Query Match 73.2%; Score 451.5; DB 2; Length 140;
        Best Local Similarity 75.2%; Pred. No. 4.6e-33;

```

QY	61	ADSVKRFETISSDSKNTAYLQMSLRADPAVYCTA----	SGY-MFAVMGGTLVTVS	115
		:   :   :   :   :   :   :   :   :   :   :		
D3	80	ADSVKRFETISSDSKNTAYLQMSLRADPAVYCTAKHDHYSNYIFDYMGGTLVTVS		139
QY	116	S	116	
D3	140	S	140	

RESULT 5  
S19666  
Ig heavy chain V region (VH3DJH4) - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #next\_change 20-Jun-2000  
C/Accession: S19666  
R/Marker: J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 223, 581-597, 1991  
A/Title: Bv-passing immunofraction. Human antibodies from V-gene libraries displayed on phage  
A/Reference number: S19663, M0ID:92085276, PMID:1748994  
A/Accession: S19666  
A/Molecule type: mRNA  
A/Residues: 1-121 <NAR>  
A/Cross-references: EMBL:X61646; NID:g37688; PIDD:CA943827.1; PID:g1335369  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F\_15-98/Domain: immunoglobulin homology <IMM>

	Query Match	73.0%	Score 450.5;	DB 2;	Length 121;
	Best Local Similarity	73.6%;	Pred. No. 4.9e-33;		
	Matches	89;	Conservative	7;	Mismatches 20; Indels 5; Gaps 1
Qy	1	EYOLVESGGGLVQPQGSRLRSCAASGFNIKOTYIHWNRQA	PGKLEWVARIDPANDNTTY	60	
	:	:::::	:::::	:::::	
Dd	1	QYOLVGSGGVVPQRSLRLRSCAASGFTFSSYGHWNRQA	PGKLEWVAITYSDGSKYY	60	
	:	:::::	:::::	:::::	
Qy	61	AADVGRFTISDDSKNTAYLQNNLSLRADTAAVVYCAGS----	*FWAVGGGLTVTS	115	
	:	:::::	:::::	:::::	
Dd	61	ADVSVGRFTISDNSKNLTLYLQNNLSLRADTAAVYCAKTGYSSGMGWCFDYWGCGILVTYS	120		

RESULT 6  
S48798  
Ig heavy chain V region (anti-Sm, VH3/DXP4/JH4b) - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S48798  
R/Kahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.  
Submitted to the EMBL Data Library, October 1994  
A/Description: Molecular characterization of natural human anti-Sm autoantibodies  
A/Reference number: S48797  
A/Accession: S48798  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-120 <MA>  
A/Cross-references: EMBL:Z46382; NID:g562324; PIDD:CAA86521.1; PIDD:g1340167  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
C/15-98/Domain: immunoglobulin homology <IM>

```

Query Match: 72.6% Score 448; DB 2; Length 120;
Best Local Similarity 74.2%; Pred. No. 8,1e-33;
Matches 89; Conservative 7; Mismatches 20; Indels 4; Gaps 2

QY      1 EVQLVESGGGLVOPGSGLRISCAASGNINIDYTHHWYRAQPGKLEWVARIDPANDNTYY 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 EVQLLESGGGLVOPGGSRLRSCAASGPTFSYAMSWVRQAPGKLEWVASISGGSGSTYY 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY      61 ADSYSGRTTISDSDSKNTATYIQNNSLAEPTTAYYYCTAS-GYRFA---YWGCGTLYTVSS 116
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```



Db 61 ADVKGRFTISRDNKNTLYLQNMNSLRAPDPAVYCAKDRGFWGKYDYGQGLTVTVSS 120

## RESULT 7

S3166 Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C/Accession: S31666

R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tommelle, C.

submitted to the EMBL Data Library, June 1992

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31666

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-138 <CUI>

A/Cross-references: EMBL:Z14202; NID:930963; PIDN:CA478571.1; PID:930964

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 447.5; DB 2; Length 138;

Best Local Similarity 74.8%; Pred. No. 1e-32;

Matches 89; Conservative 8; Mismatches 19; Indels 3; Gaps 2;

QY 1 EVOLVESGGGLVPGGSLRLISCAASGFNIDTTHHWRAQPGKLEWVARIDPANDNTIY 60

Db 20 EVOLVESGGGLVPGGSLRLISCAASGFTFSYASWVRQAPGKLEWVSALISGSGSITYY 79

QY 61 ADVKGRFTISRDNKNTLYLQNMNSLRAPDPAVYCC--TASGYW-FAWVGQGLTVTVSS 116

Db 80 ADVKGRFTISRDNKNTLYLQNMNSLRAPDPAVYCCAKARIGYVFPDMKRGTLTVTVSS 138

## RESULT 8

D36005 Ig heavy chain V region (M43) - human

C/Species: Homo sapiens (man)

C/Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Dec-1998

C/Accession: D36005

R/Schroeder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene

A/Reference number: A36005; MUID:90349571; PMID:2117273

A/Accession: D36005

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-119 <SCH>

A/Cross-references: GB:M34024

C/Genetics:

A/Gene: GDB:IGH@; IGHDI1

A/Cross-references: GDB:118731; OMIM:146910

A/Map position: 14q32.33-14q32.33

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.4%; Score 446.5; DB 2; Length 119;

Best Local Similarity 73.9%; Pred. No. 1.1e-32;

Matches 88; Conservative 7; Mismatches 21; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLISCAASGFNIDTTHHWRAQPGKLEWVARIDPANDNTIY 60

Db 1 EVOLVESGGGLVPGGSLRLISCAASGFTFSYASWVRQAPGKLEWVSALISGSGSITYY 60

QY 61 ADVKGRFTISRDNKNTLYLQNMNSLRAPDPAVYCCASGY---WFAVVGQGLTVTVSS 116

Db 61 ADVKGRFTISRDNKNTLYLQNMNSLRAPDPAVYCCAKKQNDWVFPDMKRGTLTVTVSS 119

## RESULT 9

S23624

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999

C/Accession: S23624

R/Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defeo, M.; Kozin, F.; Carson, D.A.; C

J. Exp. Med. 175, 831-842, 1992

A/Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from tv

A/Reference number: S23623; MUID:92156804; PMID:1740665

A/Accession: S23624

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-143 <OLE>

A/Cross-references: EMBL:X59703; NID:932012; PIDN:CA442224.1; PID:932013

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.4%; Score 446.5; DB 2; Length 143;

Best Local Similarity 75.2%; Pred. No. 1.3e-32;

Matches 88; Conservative 9; Mismatches 19; Indels 1; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLISCAASGFNIDTTHHWRAQPGKLEWVARIDPANDNTIY 60

Db 1 EVOLVESGGGLVPGGSLRLISCAASGFTFSYASWVRQAPGKLEWVSALISGSGSITYY 60

QY 61 ADVKGRFTISRDNKNTLYLQNMNSLRAPDPAVYCCASGYWFA-YVGQGLTVTVSS 116

Db 61 ADVKGRFTISRDNKNTLYLQNMNSLRAPDPAVYCCARSGRGSDYVGQGLTVTVSS 117

## RESULT 10

S70442 Ig heavy chain precursor V region (mu) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 21-Jan-2000

C/Accession: S70442

R/Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tommelle, C.

Mol. Immunol. 29, 1363-1373, 1992

A/Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of fet

A/Reference number: S70442; MUID:93024508; PMID:1383695

A/Accession: S70442

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-140 <CUI>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.3%; Score 446; DB 2; Length 140;

Best Local Similarity 74.2%; Pred. No. 1.4e-32;

Matches 89; Conservative 6; Mismatches 21; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLISCAASGFNIDTTHHWRAQPGKLEWVARIDPANDNTIY 60

Db 20 QVQLVESGGGLVPGGSLRLISCAASGFTFSYNGHWVRQAPGKLEWVARIFRDGSKYY 79

QY 61 ADVKGRFTISRDNKNTLYLQNMNSLRAPDPAVYCC---ASGYWFAVVGQGLTVTVSS 116

Db 80 ADVKGRFTISRDNKNTLYLQNMNSLRAPDPAVYCCARHIVGATTFDYVGQGLTVTVSS 139

## RESULT 11

S31114

Ig heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999

C/Accession: S31114

R/Rapaport, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman,

Eur. J. Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line VH3 genes and short diverse third complement

A/Reference number: S31104; MUID:92111633; PMID:1730252

A/Accession: S31114

A/Status: preliminary

A/Molecule type: mRNA

A;Residues: 1-123 <RAA>  
 A;Cross-references: EMBL:X62963  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.2%; Score 445.5; DB 2; Length 123;  
 Best Local Similarity 74.8%; Pred. No. 1.4e-32;  
 Matches 92; Conservative 6; Mismatches 18; Indels 7; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFRNIKDTYTHWROAPGKLEWVARIDPANDNTIY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFRSSYAMSWVQAQPGKLEWVAISGSGSTIY 60  
 QY 61 ADSVKGRTTISDSDSKNTAYLQNNSLRAEDTAVYYCT-ASGY-----W-FAYWGQGTLYT 113  
 DB 61 ADSVKGRTTISRDNKNTLYLQNNSLRAEDTAVYYCAKASLYLRFLEWLFDPYWGQGTLYT 120  
 QY 114 VSS 116  
 DB 121 VSS 123

RESULT 12  
 S31120  
 Ig heavy chain - human  
 C;Species: Homo sapiens (man)  
 C;Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
 C;Accession: S31120  
 R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
 Eur. J. Immunol. 22, 247-251, 1992  
 A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement  
 A;Reference number: S31104; MUID:92111633; PMID:1730252  
 A;Accession: S31120  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-114 <RAA>  
 A;Cross-references: EMBL:X62972  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.1%; Score 445; DB 2; Length 114;  
 Best Local Similarity 75.9%; Pred. No. 1.4e-32;  
 Matches 88; Conservative 9; Mismatches 17; Indels 2; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFRNIKDTYTHWROAPGKLEWVARIDPANDNTIY 60  
 DB 1 QVQLVESGGGLVQPGGSLRLSCAASGFRFSFYMSWTRQAPGKLEWVSISGSGSTIY 60  
 QY 61 ADSVKGRTTISDSDSKNTAYLQNNSLRAEDTAVYYCTASGYWFAWVGQGTLYTSS 116  
 DB 61 ADSVKGRTTISRDNKNTLYLQNNSLRAEDTAVYYC-ASGN-FDYWGQGTLYTSS 114

RESULT 13  
 S46390  
 Ig heavy chain V region - human  
 C;Species: Homo sapiens (man)  
 C;Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
 C;Accession: S46390  
 R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.  
 J. Mol. Biol. 239, 68-78, 1994  
 A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by  
 A;Reference number: S46390; MUID:94254092; PMID:8196048  
 A;Accession: S46390  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-114 <Fig>  
 A;Cross-references: EMBL:Z31686; NID:9509782; PIDN:CA83491.1; PID:g1335143  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.1%; Score 445; DB 2; Length 114;  
 Best Local Similarity 76.7%; Pred. No. 1.4e-32;  
 Matches 89; Conservative 3; Mismatches 22; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFRNIDTYTHWROAPGKLEWVARIDPANDNTIY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFRSSYAMHWROAPGKLEWVAISYDGSNKTY 60  
 QY 61 ADSVKGRTTISDSDSKNTAYLQNNSLRAEDTAVYYCTASGYWFAWVGQGTLYTSS 116  
 DB 61 ADSVKGRTTISRDNKNTLYLQNNSLRAEDTAVYYCARD--WEDYWGQGTLYTSS 114

RESULT 14  
 S30531  
 Ig heavy chain V region - human  
 C;Species: Homo sapiens (man)  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996  
 C;Accession: S30531  
 R;Marlette, X.  
 submitted to the EMBL Data Library, October 1992  
 A;Reference number: S30520  
 A;Accession: S30531  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-125 <MAR>  
 A;Cross-references: EMBL:Z18317  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.0%; Score 444.5; DB 2; Length 125;  
 Best Local Similarity 70.4%; Pred. No. 1.7e-32;  
 Matches 88; Conservative 11; Mismatches 17; Indels 9; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFRNIKDTYTHWROAPGKLEWVARIDPANDNTIY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFRSSYAMWROAPGKLEWISYISGSGSTIY 60  
 QY 61 ADSVKGRTTISDSDSKNTAYLQNNSLRAEDTAVYYCT-----ASGY---WFAWVGQGTLY 111  
 DB 61 ADSVKGRTTISRDNKNTLYLQNNSLRAEDTAVYYCARSRNYDSSGYSHYFDPYWGQGTLY 120  
 QY 112 VTYSS 116  
 DB 121 VTYSS 125

RESULT 15  
 S44111  
 Ig heavy chain V-D-J region - human  
 C;Species: Homo sapiens (man)  
 C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
 C;Accession: S44111  
 R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
 submitted to the EMBL Data Library, March 1994  
 A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable re  
 A;Reference number: S44105  
 A;Accession: S44111  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-120 <HAM>  
 A;Cross-references: EMBL:Z31387; NID:9472965; PIDN:CA83262.1; PID:9440522  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.0%; Score 444; DB 2; Length 120;  
 Best Local Similarity 72.5%; Pred. No. 1.8e-32;  
 Matches 87; Conservative 10; Mismatches 19; Indels 4; Gaps 1;

Qy 1 EVOLVESGGGLVOPGSLRLSCAASGFINIKDTYIHWVROAPGKGLEWVARIDPANDNTIY 60  
 Db 1 EVOLVESGGGVVOPGSLRLSCAASGFTPDYTMHWVROAPGKGLEWVSLISMDGSIY 60  
 Qy 61 ADSYKGRFTISSDDSKNTAYLQWNSLRAPDTAVYYC---TASGYWPAWGGTGLVTVSS 116  
 Db 61 ADSYKGRFTISRDNKNSLYLQWNSLRTEDTALYYCAKDDSSGSYYFDYWGQGTGLVTVSS 120

Search completed: May 13, 2004, 17:03:13  
 Job time : 39.875 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:38:57 ; Search time 124.875 Seconds  
(without alignments)  
244.365 Million cell updates/sec

Title: US-09-910-483-7

Perfect score: 566

Sequence: 1 DQMTQSPSSLSASVGRVT.....QQSNMPTFGQGTKEIKR 108

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: A\_Geneseq\_29Jan04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	566	100.0	108	6	ABO27262
2	566	100.0	108	6	ABO27266
3	566	100.0	108	6	ABO27278
4	566	100.0	108	6	ABO27260
5	566	100.0	108	6	ABO27258
6	566	100.0	108	6	ABO27256
7	566	100.0	108	6	ABO27264
8	557	98.4	108	6	ABO27272
9	557	98.4	108	6	ABO27270
10	557	98.4	108	6	ABO27268
11	504	89.0	105	2	AAW87458
12	504	89.0	105	2	AAW87456
13	496	87.6	108	2	AAW70622
14	496	87.6	108	2	AAW82345
15	496	87.6	108	2	ABP61191
16	496	87.6	109	5	AAU74544
17	496	87.6	110	5	AAE28149
18	495	87.5	240	4	AAAB46010
19	495	87.5	240	4	AAAB45997
20	492	86.9	240	4	AAAB46001
21	491	86.7	107	4	AAAB62087
22	491	86.7	107	4	AAAB60400
23	491	86.7	107	4	AAAB61585
24	491	86.7	107	8	AADE71454
25	489	86.4	132	2	AAW22842

26	489	86.4	240	4	AAAB6004
27	488	86.2	108	6	ABP96009
28	488	86.2	240	2	AAAY02472
29	488	86.2	240	4	AAAB5993
30	488	86.2	240	4	AAAB6040
31	488	86.2	240	4	AAAB6007
32	488	86.2	240	4	AAAB6038
33	488	86.2	240	4	AAAB6008
34	488	86.2	240	4	AAAB6005
35	488	86.2	240	4	AAAB6005
36	488	86.2	240	6	ABP95997
37	487	86.0	236	5	AAU74297
38	487	86.0	240	4	AAAB6003
39	485	85.7	240	4	AAAB6048
40	485	85.7	256	3	AAAY5072
41	485	85.7	367	3	AAAY5078
42	485	85.7	546	3	AAAY5074
43	485	85.7	626	3	AAAY5081
44	484	85.5	107	2	AAAR30770
45	484	85.5	109	2	AAAR47041

## ALIGNMENTS

RESULT 1	ABO27262	standard; protein; 108 AA.
ID	ABO27262	standard; protein; 108 AA.
XX	ABO27262;	
AC	ABO27262;	
DT	23-OCT-2003	(revised)
DT	11-SEP-2003	(first entry)
XX	ICAM-1 binding humanised antibody Humd VL domain.	
XX	Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;	
KW	human rhinovirus; human coxsackievirus; protozoa; malaria; infection;	
KW	respiratory syncytial virus; fungi; antibody; humanised antibody.	
XX	Mus sp.	
OS	Homo sapiens.	
OS	Chimeric.	
XX	US2003035798-A1.	
XX	20-FEB-2003.	
XX	19-JUL-2001; 2001US-00910483.	
XX	30-NOV-1998; 98NO-US025422.	
XX	16-AUG-2000; 2000US-00555476.	
XX	(FANG/) FANG F.	
XX	(KOH/) KOHSTAEDT L.	
XX	(RENO/) RENO J.	
XX	Fang F, Kohlstadt L, Reno J;	
XX	WPI; 2003-503356/47.	
XX	New humanized antibody binding ICAM-1 and/or inhibits pathogen infection	
XX	of cells expressing ICAM-1, useful for treating infection caused by HRV,	
XX	coxsackie A virus, respiratory syncytial virus, bacteria, fungi and	
XX	protozoa.	
XX	Claim 1; Page 18; 30pp; English.	
XX	The invention relates to a humanised antibody that binds intracellular	
XX	adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells	
XX	expressing ICAM-1, comprising any of the fully defined Huma to Humt	
XX	sequences. The methods and compositions are useful for inhibiting	
XX	infection and/or progression of infection caused by pathogens such as	



QY 1 DIQWTSPPSSLSASVGDVGVITTCRASQISNNLHMWYQKPKAKLLIYHASQISGVPS 60  
DB 1 DIQWTSPPSSLSASVGDVGVITTCRASQISNNLHMWYQKPKAKLLIYHASQISGVPS 60  
QY 61 RFGSGSGGTDFTLTISLQPEDFATYCCQOSNSMPYTFGGGTKEIKR 108  
DB 61 RFGSGSGGTDFTLTISLQPEDFATYCCQOSNSMPYTFGGGTKEIKR 108  
RESULT 4  
ABO27260 standard; protein; 108 AA.  
ABO27260  
AC ABO27260;  
XX  
XX 23-OCT-2003 (revised)  
DT 11-SEP-2003 (first entry)  
DE ICAM-1 binding humanised antibody HumC vL domain.  
XX  
XX Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;  
KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;  
XX respiratory syncytial virus; fungi; antibody; humanised antibody.  
XX  
XX Mus sp.  
OS Homo sapiens.  
OS Chimeric.  
XX  
XX US2003035798-A1.  
PN 20-FEB-2003.  
PD 19-JUL-2001; 2001US-00910483.  
PF 30-NOV-1998; 98WO-US025422.  
PR 16-AUG-2000; 2000US-00555446.  
XX  
XX (FANG/) FANG F.  
PA (KOH/) KOHLSTAEDE L.  
XX (RENO/) RENO J.  
PI Fang F, Kohlstaedt L, Reno J;  
XX WPI; 2003-503356/47.  
DR New humanized antibody binding ICAM-1 and/or inhibits pathogen infection  
XX of cells expressing ICAM-1, useful for treating infection caused by HRV,  
PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and  
XX protozoa.  
XX  
XX Claim 1; Page 18; 30pp; English.  
PS The invention relates to a humanised antibody that binds intracellular  
XX adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells  
CC expressing ICAM-1, comprising any of the fully defined HumA to HumL  
CC sequences. The methods and compositions are useful for inhibiting  
XX infection and/or progression of infection caused by pathogens such as  
CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,  
CC bacteria, fungi and protozoa, in particular malaria. The present sequence  
CC represents the amino acid sequence of ICAM-1 binding humanised antibody  
XX domain. (Updated on 23-Oct-2003 to standardise OS field)  
XX  
SQ Sequence 108 AA;  
Query Match 100.0%; Score 566; DB 6; Length 108;  
Best Local Similarity 100.0%; Pred. No. 2e-31;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DIQWTSPPSSLSASVGDVGVITTCRASQISNNLHMWYQKPKAKLLIYHASQISGVPS 60  
DB 1 DIQWTSPPSSLSASVGDVGVITTCRASQISNNLHMWYQKPKAKLLIYHASQISGVPS 60

QY 61 RFGSGSGGTDFTLTISLQPEDFATYCCQOSNSMPYTFGGGTKEIKR 108  
DB 61 RFGSGSGGTDFTLTISLQPEDFATYCCQOSNSMPYTFGGGTKEIKR 108  
RESULT 5  
ABO27258 standard; protein; 108 AA.  
ABO27258  
AC ABO27258;  
XX  
XX 23-OCT-2003 (revised)  
DT 11-SEP-2003 (first entry)  
DE ICAM-1 binding humanised antibody HumB vL domain.  
XX  
XX Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;  
KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;  
XX respiratory syncytial virus; fungi; antibody; humanised antibody.  
XX  
XX Mus sp.  
OS Homo sapiens.  
OS Chimeric.  
XX  
XX US2003035798-A1.  
PN 20-FEB-2003.  
PD 19-JUL-2001; 2001US-00910483.  
PF 30-NOV-1998; 98WO-US025422.  
PR 16-AUG-2000; 2000US-00555446.  
XX  
XX (FANG/) FANG F.  
PA (KOH/) KOHLSTAEDE L.  
XX (RENO/) RENO J.  
PI Fang F, Kohlstaedt L, Reno J;  
XX WPI; 2003-503356/47.  
DR New humanized antibody binding ICAM-1 and/or inhibits pathogen infection  
XX of cells expressing ICAM-1, useful for treating infection caused by HRV,  
PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and  
XX protozoa.  
XX  
XX Claim 1; Page 17; 30pp; English.  
PS The invention relates to a humanised antibody that binds intracellular  
XX adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells  
CC expressing ICAM-1, comprising any of the fully defined HumA to HumL  
CC sequences. The methods and compositions are useful for inhibiting  
XX infection and/or progression of infection caused by pathogens such as  
CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,  
CC bacteria, fungi and protozoa, in particular malaria. The present sequence  
CC represents the amino acid sequence of ICAM-1 binding humanised antibody  
XX domain. (Updated on 23-Oct-2003 to standardise OS field)  
XX  
SQ Sequence 108 AA;  
Query Match 100.0%; Score 566; DB 6; Length 108;  
Best Local Similarity 100.0%; Pred. No. 2e-31;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DIQWTSPPSSLSASVGDVGVITTCRASQISNNLHMWYQKPKAKLLIYHASQISGVPS 60  
DB 1 DIQWTSPPSSLSASVGDVGVITTCRASQISNNLHMWYQKPKAKLLIYHASQISGVPS 60  
QY 61 RFGSGSGGTDFTLTISLQPEDFATYCCQOSNSMPYTFGGGTKEIKR 108  
DB 61 RFGSGSGGTDFTLTISLQPEDFATYCCQOSNSMPYTFGGGTKEIKR 108

## RESULT 6

ABO27256 standard; protein; 108 AA.

ABO27256;

23-OCT-2003 (revised)  
11-SEP-2003 (first entry)

ICAM-1 binding humanised antibody Huma VL domain.

Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;  
human rhinovirus; human coxsackievirus; protozoa; malaria; infection;  
respiratory syncytial virus; fungi; antibody; humanised antibody.Mus sp.  
Homo sapiens.  
Chimeric.

US2003035298-A1

20-FEB-2003.

19-JUL-2001; 2001US-00910483.

30-NOV-1998; 98WO-US025422.

16-AUG-2000; 2000US-00555446.

(FANG/) FANG F.  
(KOH/) KOHLSTADT L.  
(RENO/) RENO J.

Fang F, Kohlstaedt L, Reno J;

WPI; 2003-503356/47.

New humanized antibody binding ICAM-1 and/or inhibits pathogen infection  
of cells expressing ICAM-1, useful for treating infection caused by HRV,  
coxsackie A virus, respiratory syncytial virus, bacteria, fungi and  
protozoa.

Claim 1; Page 17; 30pp; English.

The invention relates to a humanised antibody that binds intracellular  
adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells  
expressing ICAM-1, comprising any of the fully defined Huma to Humt  
sequences. The methods and compositions are useful for inhibiting  
infection and/or progression of infection caused by pathogens such as  
human rhinovirus, coxsackie A virus, respiratory syncytial virus,  
bacteria, fungi and protozoa, in particular malaria. The present sequence  
represents the amino acid sequence of ICAM-1 binding humanised antibody  
domain. (Updated on 23-OCT-2003 to standardise OS field)

Sequence 108 AA;

Query Match 100.0%; Score 566; DB 6; Length 108;

Best Local Similarity 100.0%; Pred. No. 2e-31;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DIQWTQSPSSLSASVGDRTVITTCRASQISNNLHMWYQKRGKAPKLLIYHSAOSISGVPS	60
DB	1	DIQWTQSPSSLSASVGDRTVITTCRASQISNNLHMWYQKRGKAPKLLIYHSAOSISGVPS	60
QY	61	RFGSGSGGTDFTLTISLQPEDPATYTCQOSNWPYTFGGGTVEIKR	108
DB	61	RFGSGSGGTDFTLTISLQPEDPATYTCQOSNWPYTFGGGTVEIKR	108

## RESULT 7

ABO27264 standard; protein; 108 AA.

ABO27264;

23-OCT-2003 (revised)  
11-SEP-2003 (first entry)

ICAM-1 binding humanised antibody Hume VL domain.

Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;  
human rhinovirus; human coxsackievirus; protozoa; malaria; infection;  
respiratory syncytial virus; fungi; antibody; humanised antibody.Mus sp.  
Homo sapiens.  
Chimeric.

US2003035298-A1

20-FEB-2003.

19-JUL-2001; 2001US-00910483.

30-NOV-1998; 98WO-US025422.

16-AUG-2000; 2000US-00555446.

(FANG/) FANG F.  
(KOH/) KOHLSTADT L.  
(RENO/) RENO J.

Fang F, Kohlstaedt L, Reno J;

WPI; 2003-503356/47.

New humanized antibody binding ICAM-1 and/or inhibits pathogen infection  
of cells expressing ICAM-1, useful for treating infection caused by HRV,  
coxsackie A virus, respiratory syncytial virus, bacteria, fungi and  
protozoa.

Claim 1; Page 18-19; 30pp; English.

The invention relates to a humanised antibody that binds intracellular  
adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells  
expressing ICAM-1, comprising any of the fully defined Huma to Humt  
sequences. The methods and compositions are useful for inhibiting  
infection and/or progression of infection caused by pathogens such as  
human rhinovirus, coxsackie A virus, respiratory syncytial virus,  
bacteria, fungi and protozoa, in particular malaria. The present sequence  
represents the amino acid sequence of ICAM-1 binding humanised antibody  
domain. (Updated on 23-OCT-2003 to standardise OS field)

Sequence 108 AA;

Query Match 100.0%; Score 566; DB 6; Length 108;

Best Local Similarity 100.0%; Pred. No. 2e-31;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DIQWTQSPSSLSASVGDRTVITTCRASQISNNLHMWYQKRGKAPKLLIYHSAOSISGVPS	60
DB	1	DIQWTQSPSSLSASVGDRTVITTCRASQISNNLHMWYQKRGKAPKLLIYHSAOSISGVPS	60
QY	61	RFGSGSGGTDFTLTISLQPEDPATYTCQOSNWPYTFGGGTVEIKR	108
DB	61	RFGSGSGGTDFTLTISLQPEDPATYTCQOSNWPYTFGGGTVEIKR	108

## RESULT 8

ABO27272 standard; protein; 108 AA.

ABO27272;

23-OCT-2003 (revised)

11-SEP-2003 (first entry)

ICAM-1 binding humanised antibody Humi VL domain.



XX Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;  
 KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;  
 KM respiratory syncytial virus; fungi; antibody; humanised antibody.  
 OS Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX US2003035798-A1.  
 XX PD 20-FEB-2003.  
 XX PF 19-JUL-2001; 2001US-00910483.  
 XX PR 30-NOV-1998; 98WO-US025422.  
 XX PR 16-AUG-2000; 2000US-00555446.  
 XX PA (FANG/) FANG F.  
 XX PA (KOH/) KOHLSTADT L.  
 XX PA (RENO/) RENO J.  
 XX PI Fang F, Kohlstaedt L, RENO J;  
 XX DR WPI; 2003-503356/47.  
 XX PT New humanized antibody binding ICAM-1 and/or inhibits pathogen infection  
 PT of cells expressing ICAM-1, useful for treating infection caused by HRV,  
 PT coxackie A virus, respiratory syncytial virus, bacteria, fungi and  
 PT protozoa.  
 XX PS Claim 1; Page 20; 30pp; English.  
 CC The invention relates to a humanised antibody that binds intracellular  
 CC adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells  
 CC expressing ICAM-1, comprising any of the fully defined Huma to Humt  
 CC sequences. The methods and compositions are useful for inhibiting  
 CC infection and/or progression of infection caused by pathogens such as  
 CC human rhinovirus, coxackie A virus, respiratory syncytial virus,  
 CC bacteria, fungi and protozoa, in particular malaria. The present sequence  
 CC represents the amino acid sequence of ICAM-1 binding humanised antibody  
 CC domain. (Updated on 23-Oct-2003 to standardise OS field)  
 XX SO Sequence 108 AA;  
 Query Match 98.4%; Score 557; DB 6; Length 108;  
 Best Local Similarity 99.1%; Pred. No. 8e-31;  
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVITTCRASQISINNLHWYQOKGKAPKLIYHASQISIGVPS 60  
 DB 1 DIQMTQSPSSLSASVGRVITTCRASQISINNLHWYQOKGKAPKLIYHASQISIGVPS 60  
 QY 61 RFGSGSGGTDFLTITISLQPEDFATYYCOQSNMPTFFGGGTKEIKR 108  
 DB 61 RFGSGSGGTDFLTITISLQPEDFATYYCOQSNMPTFFGGGTKEIKR 108  
 RESULT 9  
 ID ABO27270 standard; protein; 108 AA.  
 XX ABO27270;  
 XX AC ABO27270;  
 XX DT 23-OCT-2003 (revised)  
 XX DT 11-SEP-2003 (first entry)  
 XX DE ICAM-1 binding humanised antibody HumH VL domain.  
 XX KW Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;  
 KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;  
 KM respiratory syncytial virus; fungi; antibody; humanised antibody.  
 XX

OS Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX US2003035798-A1.  
 XX PD 20-FEB-2003.  
 XX PF 19-JUL-2001; 2001US-00910483.  
 XX PR 30-NOV-1998; 98WO-US025422.  
 XX PR 16-AUG-2000; 2000US-00555446.  
 XX PA (FANG/) FANG F.  
 XX PA (KOH/) KOHLSTADT L.  
 XX PA (RENO/) RENO J.  
 XX PI Fang F, Kohlstaedt L, RENO J;  
 XX DR WPI; 2003-503356/47.  
 XX PT New humanized antibody binding ICAM-1 and/or inhibits pathogen infection  
 PT of cells expressing ICAM-1, useful for treating infection caused by HRV,  
 PT coxackie A virus, respiratory syncytial virus, bacteria, fungi and  
 PT protozoa.  
 XX PS Claim 1; Page 20; 30pp; English.  
 CC The invention relates to a humanised antibody that binds intracellular  
 CC adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells  
 CC expressing ICAM-1, comprising any of the fully defined Huma to Humt  
 CC sequences. The methods and compositions are useful for inhibiting  
 CC infection and/or progression of infection caused by pathogens such as  
 CC human rhinovirus, coxackie A virus, respiratory syncytial virus,  
 CC bacteria, fungi and protozoa, in particular malaria. The present sequence  
 CC represents the amino acid sequence of ICAM-1 binding humanised antibody  
 CC domain. (Updated on 23-Oct-2003 to standardise OS field)  
 XX SO Sequence 108 AA;  
 Query Match 98.4%; Score 557; DB 6; Length 108;  
 Best Local Similarity 99.1%; Pred. No. 8e-31;  
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVITTCRASQISINNLHWYQOKGKAPKLIYHASQISIGVPS 60  
 DB 1 DIQMTQSPSSLSASVGRVITTCRASQISINNLHWYQOKGKAPKLIYHASQISIGVPS 60  
 QY 61 RFGSGSGGTDFLTITISLQPEDFATYYCOQSNMPTFFGGGTKEIKR 108  
 DB 61 RFGSGSGGTDFLTITISLQPEDFATYYCOQSNMPTFFGGGTKEIKR 108  
 RESULT 10  
 ID ABO27268 standard; protein; 108 AA.  
 XX ABO27268;  
 XX AC ABO27268;  
 XX DT 23-OCT-2003 (revised)  
 XX DT 11-SEP-2003 (first entry)  
 XX DE ICAM-1 binding humanised antibody HumH VL domain.  
 XX KW Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;  
 KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;  
 KM respiratory syncytial virus; fungi; antibody; humanised antibody.  
 XX Mus sp.  
 XX OS Homo sapiens.  
 XX OS Chimeric.  
 XX PN US2003035798-A1.

```

XX 20-FEB-2003.
PD
XX
PF 19-JUL-2001; 2001US-00910483.
XX
XX 30-NOV-1998; 98WO-US025422.
XX 16-AUG-2000; 2000US-00555446.
XX
PA (FANG/) FANG F.
PA (KOH/) KOHLSTADT L.
PA (RENO/) RENO J.
PI Fang F, Kohlstaedt L, Reno J;
PI WPI; 2003-503356/47.
XX
XX New humanized antibody binding ICAM-1 and/or inhibits pathogen infection
PT of cells expressing ICAM-1, useful for treating infection caused by HRV,
PT coxackie A virus, respiratory syncytial virus, bacteria, fungi and
PT protozoa.
XX
PS Claim 1; Page 19; 30pp; English.
XX
CC The invention relates to a humanised antibody that binds intracellular
CC adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells
CC expressing ICAM-1, comprising any of the fully defined Huma to Humi
CC sequences. The methods and compositions are useful for inhibiting
CC infection and/or progression of infection caused by pathogens such as
CC human rhinovirus, coxackie A virus, respiratory syncytial virus,
CC bacteria, fungi and protozoa, in particular malaria. The present sequence
CC represents the amino acid sequence of ICAM-1 binding humanised antibody
CC domain. (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 108 AA;
XX
Query Match 98.4%; Score 557; DB 6; Length 108;
Best Local Similarity 99.1%; Pred. No. 8e-31;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 DIOMTOSPSLSASVGDRTVITTCRASQISNNLHWYQKRGKAPKLLIYHASQISGVPS 60
DB 1 DIOMTOSPSLSASVGDRTVITTCRASQISNNLHWYQKRGKAPKLLIYHASQISGVPS 60
XX
QY 61 RFGSGSGGTDFTLTISLSLOPEDPATYTCQOSNSWPYTFGQGTVEIKR 108
DB 61 RFGSGSGGTDFTLTISLSLOPEDPATYTCQOSNSWPYTFGQGTVEIKR 108
XX
RESULT 11
AAW87456
ID AAW87456 standard; protein; 105 AA.
XX
AC AAW87456;
XX
DT 15-MAR-1999 (first entry)
XX
DE Jk gene product.
XX
XX Humanised antibody; monoclonal antibody; MAb; antibody engineering;
XX mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer;
XX metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis;
XX diabetic retinopathy; inflammation; macular degeneration; osteoporosis;
XX Paget's disease; hyperparathyroidism; hypercalcaemia; therapy;
XX immunotherapy; D1ZHREI; Jk protein.
XX
XX Mus sp.
XX OS
XX PN WO9840488-A1.
XX
XX PD 17-SEP-1998.
XX
XX PF 12-MAR-1998; 98WO-US004987.
XX
XX

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PR 12-MAR-1997; 97US-0039609P.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Jonak ZL, Johanson KO, Taylor AH;
XX
XX WPI; 1999-034590/03.
XX DR N-PSDB; AAV71803.
XX
XX New anti alpha.v beta.3 vitronectin receptor antibodies - used for
PT immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory
PT disorders, atherosclerosis, restenosis, cancers or osteoporosis.
XX
XX Example 14; Page 66; 97pp; English.
XX
XX This polypeptide is encoded by a Jk synthetic gene segment (see
CC AAV71803). It was utilising in novel D1ZHREI humanised light chain
CC variable region (see AAW87458), which comprises a human REI framework and
CC complementarity determining regions from the anti-human alpha-v beta-3
CC vitronectin receptor monoclonal antibody D12. Humanised D12 antibodies
CC can be used for passive immunotherapy of disorders mediated by the alpha-
CC v beta-3 vitronectin receptor, e.g. restenosis and angiogenic associated
CC diseases
XX
SQ Sequence 105 AA;
XX
Query Match 89.0%; Score 504; DB 2; Length 105;
Best Local Similarity 90.5%; Pred. No. 3.1e-27;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 DIOMTOSPSLSASVGDRTVITTCRASQISNNLHWYQKRGKAPKLLIYHASQISGVPS 60
DB 1 DIVLTQSPSLSASVGDRTVITTCRASQISNNLHWYQKRGKAPKLLIYHASQISGVPS 60
XX
QY 61 RFGSGSGGTDFTLTISLSLOPEDPATYTCQOSNSWPYTFGQGTVEIKR 105
DB 61 RFGSGSGGTDFTLTISLSLOPEDPATYTCQOSNSWPYTFGQGTVEIKR 105
XX
RESULT 12
AAW87458
ID AAW87458 standard; protein; 105 AA.
XX
AC AAW87458;
XX
DT 15-MAR-1999 (first entry)
XX
DE Humanised anti-alpha.v beta-3 MAb D1ZHLCREI VL.
XX
XX Humanised antibody; monoclonal antibody; MAb; antibody engineering;
XX mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer;
XX metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis;
XX diabetic retinopathy; inflammation; macular degeneration; osteoporosis;
XX Paget's disease; hyperparathyroidism; hypercalcaemia; therapy;
XX immunotherapy; D1ZHLCREI.
XX
XX Homo sapiens.
XX OS
XX PN WO9840488-A1.
XX
XX PD 17-SEP-1998.
XX
XX PF 12-MAR-1998; 98WO-US004987.
XX
XX PR 12-MAR-1997; 97US-0039609P.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Jonak ZL, Johanson KO, Taylor AH;
XX
XX WPI; 1999-034590/03.
XX DR N-PSDB; AAV71805.
XX

```

XX New anti alpha v beta 3 vitronectin receptor antibodies - used for  
PT immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory  
PT disorders, atherosclerosis, restenosis, cancers or osteoporosis.

XX Example 14; Page 68-69; 97pp; English.

XX This is the amino acid sequence of the light chain variable region (VL)  
CC of humanised anti-alpha-v beta-3 vitronectin receptor monoclonal antibody  
CC DIH2H2CREI. It is based on a synthetic humanised kappa chain based on a  
CC modified human HBI kappa framework and complementarity determining  
CC regions from the murine anti-human alpha-v beta-3 vitronectin receptor  
CC monoclonal antibody D12 (see AAW84094). Humanised antibodies of the  
CC invention can be used for passive immunotherapy of a disorder mediated by  
CC the alpha-v beta-3 receptor, e.g. cardiovascular disorders or angiogenic-  
CC related disorders, such as angiogenesis associated with diabetic  
CC retinopathy, atherosclerosis and restenosis, chronic inflammatory  
CC disorders, macular degeneration, rheumatoid arthritis and cancer, e.g.  
CC solid tumour metastasis, and diseases where bone resorption is associated  
CC with pathology such as osteoporosis, hyperparathyroidism, Paget's  
CC disease, hypercalcaemia of malignancy, osteolytic lesions produced by bone  
CC metastasis, bone loss due to immobilisation or sex hormone deficiency.  
CC They can also be used for targeted drug therapy, and for detection and  
CC diagnosis

XX Sequence 105 AA;

Query Match 89.0%; Score 504; DB 2; Length 105;  
Best Local Similarity 90.5%; Pred. No. 3.1e-27;  
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDRTVITTCRASQSSINNLHMVYQKPKAPKLLIYHASSQISGVPS 60  
DB 1 DIVLQSPSSLSASVGDRTVITTCRASQSSINNLHMVYQKPKAPKLLIYHASSQISGVPS 60  
QY 61 RFGSGSGGTDFTLTSSLOPEDFATYYCCQSNMWPYFGQTKVEIR 105  
DB 61 RFGSGSGGTDFTLTSSLOPEDFATYYCCQSNMWPYFGQTKVEIR 105

RESULT 13  
AAW70622  
ID AAW70622 standard; peptide; 108 AA.

XX AC AAW70622;

XX DT 27-JAN-1999 (first entry)

XX Human consensus framework hum kappa1 for light kappa subgroup 1.

XX Light variable domain; murine; humanised antibody;  
XX anti-vascular endothelial growth factor antibody; anti-VEGF antibody;  
XX VEGF-induced angiogenesis; tumour; retinal disorder;  
XX age-related macular degeneration; diabetic retinopathy;  
XX rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease;  
XX Human consensus framework hum kappa1; light kappa subgroup 1.

XX Homo sapiens.

XX MO9845331-A2.

XX 15-OCT-1998.

XX 03-APR-1998; 98WO-US0006604.

XX 07-APR-1997; 97US-00833504.

XX 06-AUG-1997; 97US-00908469.

XX (GETH ) GENENTECH INC.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI; 1998-568337/48.

XX New humanised antibody with affinity for vascular endothelial growth  
PT factor - for treatment of tumours, retinal disease and other angiogenic  
PT states, also related nucleic acid, vectors and transformed cells.

XX Example 1; Fig 1B; 100pp; English.

XX The present sequence represents the human consensus framework hum kappa1  
CC for light kappa subgroup 1. The sequence is used to humanise the variable  
CC light domain of the murine anti-vascular endothelial growth factor (anti-  
CC VEGF) antibody A4.6.1. The humanised antibodies are used to inhibit VEGF  
CC -induced angiogenesis, particularly for treating or preventing tumours  
CC (of any type) and retinal disorders (e.g. age-related macular  
CC degeneration or diabetic retinopathy). They can also be used to treat  
CC other conditions that involve angiogenesis, e.g. rheumatoid arthritis,  
CC psoriasis, atherosclerosis, Grave's disease, etc

XX Sequence 108 AA;

Query Match 87.6%; Score 496; DB 2; Length 108;  
Best Local Similarity 91.7%; Pred. No. 1.1e-26;  
Matches 99; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDRTVITTCRASQSSINNLHMVYQKPKAPKLLIYHASSQISGVPS 60  
DB 1 DIVLQSPSSLSASVGDRTVITTCRASQSSINNLHMVYQKPKAPKLLIYHASSQISGVPS 60  
QY 61 RFGSGSGGTDFTLTSSLOPEDFATYYCCQSNMWPYFGQTKVEIR 108  
DB 61 RFGSGSGGTDFTLTSSLOPEDFATYYCCQSNMWPYFGQTKVEIR 108

RESULT 14  
AA82345  
ID AA82345 standard; protein; 108 AA.

XX AC AA82345;

XX DT 22-JUN-2000 (first entry)

XX Human consensus sequence of light chain subgroup KI SEQ ID NO:3.

XX Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;  
XX antitumour; antiviral; inflammation; immunological response; LPA-1;  
XX lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;  
XX inflammatory bowel disease; systemic lupus erythematosus; leukaemia;  
XX viral infection; transplant rejection; graft rejection.

XX Homo sapiens.

XX US6037454-A.

XX 14-MAR-2000.

XX 20-NOV-1997; 97US-00974899.

XX 27-NOV-1996; 96US-0031971P.

XX (GETH ) GENENTECH INC.

XX Jardieu PM, Presta LG;

XX WPI; 2000-282241/24.

XX New humanized anti-CD11a antibody, useful for treating or preventing e.g.  
PT inflammation and transplant rejection, contains human heavy variable  
PT region complementarity determining regions.

XX Example; Fig 1; 38pp; English.

XX The present invention describes a humanised anti-CD11a antibody (Ab) that  
CC binds specifically to the human CD11a I-domain. The Ab has anti-  
CC inflammatory, immunosuppressant, antitumour and antiviral activities. The





CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,  
CC bacteria, fungi and protozoa, in particular malaria. The present sequence  
CC represents the amino acid sequence of a humanised antibody 1A6 domain.  
CC (Updated on 23-OCT-2003 to standardise OS field)

XX Sequence 116 AA;

Query Match 100.0%; Score 617; DB 6; Length 116;  
Best Local Similarity 100.0%; Pred. No. 2,1e-47;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60  
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60

QY 61 ADSVKGFRFTISSDSSKNTAVLQNNSLRAEDTAVYYCTASGYWPAWVGQGLTVTVSS 116  
DB 61 ADSVKGFRFTISSDSSKNTAVLQNNSLRAEDTAVYYCTASGYWPAWVGQGLTVTVSS 116

#### RESULT 2

ABO27257 standard; protein; 116 AA.

AC ABO27257;  
DT 23-OCT-2003 (revised)  
DT 11-SEP-2003 (first entry)

DE ICM-1 binding humanised antibody HumB vH domain.

KW Human; mouse; ICM-1; intracellular adhesion molecule-1; bacteria;  
KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;  
KW respiratory syncytial virus; fungi; antibody; humanised antibody.

OS Mus sp.  
OS Homo sapiens.  
OS Chimeric.

PN US2003035798-A1.

XX 20-FEB-2003.

XX 19-JUL-2001; 2001US-00910483.

XX 30-NOV-1998; 98WO-US025422.

XX 16-AUG-2000; 2000US-00555446.

PA (FANG/) FANG F.  
PA (KOHL/) KOHLSTADT L.  
PA (RENO/) RENO J.

PI Fang F, Kohlstaedt L, Reno J;

DR WPI; 2003-503356/47.

PT New humanized antibody binding ICM-1 and/or inhibits pathogen infection  
PT of cells expressing ICM-1, useful for treating infection caused by HRV,  
PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and  
PT protozoa.

PS Claim 1; Page 17; 30pp; English.

CC The invention relates to a humanised antibody that binds intracellular  
CC adhesion molecule-1, ICM-1 and/or inhibits pathogen infection of cells  
CC expressing ICM-1, comprising any of the fully defined HumA to HumI  
CC sequences. The methods and compositions are useful for inhibiting  
CC infection and/or progression of infection caused by pathogens such as  
CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,  
CC bacteria, fungi and protozoa, in particular malaria. The present sequence  
CC represents the amino acid sequence of ICM-1 binding humanised antibody  
CC domain. (Updated on 23-OCT-2003 to standardise OS field)

SQ Sequence 116 AA;

Query Match 100.0%; Score 617; DB 6; Length 116;  
Best Local Similarity 100.0%; Pred. No. 2,1e-47;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60  
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60

QY 61 ADSVKGFRFTISSDSSKNTAVLQNNSLRAEDTAVYYCTASGYWPAWVGQGLTVTVSS 116  
DB 61 ADSVKGFRFTISSDSSKNTAVLQNNSLRAEDTAVYYCTASGYWPAWVGQGLTVTVSS 116

#### RESULT 3

ABO27261 standard; protein; 116 AA.

AC ABO27261;

DT 23-OCT-2003 (revised)  
DT 11-SEP-2003 (first entry)

DE ICM-1 binding humanised antibody HumB vH domain.

KW Human; mouse; ICM-1; intracellular adhesion molecule-1; bacteria;  
KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;  
KW respiratory syncytial virus; fungi; antibody; humanised antibody.

OS Mus sp.  
OS Homo sapiens.  
OS Chimeric.

PN US2003035798-A1.

XX 20-FEB-2003.

XX 19-JUL-2001; 2001US-00910483.

XX 30-NOV-1998; 98WO-US025422.

XX 16-AUG-2000; 2000US-00555446.

PA (FANG/) FANG F.  
PA (KOHL/) KOHLSTADT L.  
PA (RENO/) RENO J.

PI Fang F, Kohlstaedt L, Reno J;

DR WPI; 2003-503356/47.

PT New humanized antibody binding ICM-1 and/or inhibits pathogen infection  
PT of cells expressing ICM-1, useful for treating infection caused by HRV,  
PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and  
PT protozoa.

PS Claim 1; Page 18; 30pp; English.

CC The invention relates to a humanised antibody that binds intracellular  
CC adhesion molecule-1, ICM-1 and/or inhibits pathogen infection of cells  
CC expressing ICM-1, comprising any of the fully defined HumA to HumI  
CC sequences. The methods and compositions are useful for inhibiting  
CC infection and/or progression of infection caused by pathogens such as  
CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,  
CC bacteria, fungi and protozoa, in particular malaria. The present sequence  
CC represents the amino acid sequence of ICM-1 binding humanised antibody  
CC domain. (Updated on 23-OCT-2003 to standardise OS field)

SQ Sequence 116 AA;

Query Match 99.4%; Score 613; DB 6; Length 116;  
Best Local Similarity 99.1%; Pred. No. 4,8e-47;  
Matches 115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVDPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60  
DB 1 EVOLVESGGGLVDPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60

QY 61 ADSVKGKFTTSSDSSKNTATYLONNSLRAEDTAVYYCTASGWPAYWGQGLTVTVSS 116  
DB 61 ADSVKGKFTTSSDSSKNTATYLONNSLRAEDTAVYYCTTSGWFPAYWGQGLTVTVSS 116

RESULT 4  
ID ABO27255 standard; protein: 116 AA.  
AC ABO27255;  
XX  
XX 23-OCT-2003 (revised)  
DT 11-SEP-2003 (first entry)  
XX  
XX ICM-1 binding humanised antibody huma vH domain.  
DE  
XX Human; mouse; ICM-1; intracellular adhesion molecule-1; bacteria;  
KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;  
KW respiratory syncytial virus; fungi; antibody; humanised antibody.  
XX  
XX Mus sp.  
OS Homo sapiens.  
OS Chimeric.  
XX  
XX US2003035798-A1.  
XX  
XX 20-FEB-2003.  
XX  
XX 19-JUL-2001; 2001US-00910483.  
PF 30-NOV-1998; 98WO-US025422.  
PR 16-AUG-2000; 2000US-00555446.  
XX  
XX (FANG/) FANG F.  
PA (KOH/) KOHLSTAEDT L.  
XX (RENO/) RENO J.  
XX  
XX Fang F, Kohlstaedt L, RENO J;  
PI  
XX WPI; 2003-503356/47.  
DR  
XX New humanized antibody binding ICM-1 and/or inhibits pathogen infection  
PT of cells expressing ICM-1, useful for treating infection caused by HRV,  
PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and  
PT protozoa.  
XX  
XX Claim 1; Page 17; 30pp; English.  
PS  
XX The invention relates to a humanised antibody that binds intracellular  
CC adhesion molecule-1, ICM-1 and/or inhibits pathogen infection of cells  
CC expressing ICM-1, comprising any of the fully defined huma to Humt  
CC sequences. The methods and compositions are useful for inhibiting  
CC infection and/or progression of infection caused by pathogens such as  
CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,  
CC bacteria, fungi and protozoa, in particular malaria. The present sequence  
CC represents the amino acid sequence of ICM-1 binding humanised antibody  
CC domain. (Updated on 23-Oct-2003 to standardise OS field)  
XX  
XX  
SQ Sequence 116 AA;  
Query Match 99.0%; Score 611; DB 6; Length 116;  
Best Local Similarity 99.1%; Pred. No. 7.3e-47;  
Matches 115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVDPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60  
DB 1 EVOLVESGGGLVDPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60

QY 61 ADSVKGKFTTSSDSSKNTATYLONNSLRAEDTAVYYCTASGWPAYWGQGLTVTVSS 116  
DB 61 ADSVKGKFTTSSDSSKNTATYLONNSLRAEDTAVYYCTDSGWFPAYWGQGLTVTVSS 116

RESULT 5  
ID ABO27267 standard; protein: 116 AA.  
AC ABO27267;  
XX  
XX 23-OCT-2003 (revised)  
DT 11-SEP-2003 (first entry)  
XX  
XX ICM-1 binding humanised antibody humg vH domain.  
DE  
XX Human; mouse; ICM-1; intracellular adhesion molecule-1; bacteria;  
KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;  
KW respiratory syncytial virus; fungi; antibody; humanised antibody.  
XX  
XX Mus sp.  
OS Homo sapiens.  
OS Chimeric.  
XX  
XX US2003035798-A1.  
XX  
XX 20-FEB-2003.  
XX  
XX 19-JUL-2001; 2001US-00910483.  
PF 30-NOV-1998; 98WO-US025422.  
PR 16-AUG-2000; 2000US-00555446.  
XX  
XX (FANG/) FANG F.  
PA (KOH/) KOHLSTAEDT L.  
XX (RENO/) RENO J.  
XX  
XX Fang F, Kohlstaedt L, RENO J;  
PI  
XX WPI; 2003-503356/47.  
DR  
XX New humanized antibody binding ICM-1 and/or inhibits pathogen infection  
PT of cells expressing ICM-1, useful for treating infection caused by HRV,  
PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and  
PT protozoa.  
XX  
XX Claim 1; Page 19; 30pp; English.  
PS  
XX The invention relates to a humanised antibody that binds intracellular  
CC adhesion molecule-1, ICM-1 and/or inhibits pathogen infection of cells  
CC expressing ICM-1, comprising any of the fully defined huma to Humt  
CC sequences. The methods and compositions are useful for inhibiting  
CC infection and/or progression of infection caused by pathogens such as  
CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,  
CC bacteria, fungi and protozoa, in particular malaria. The present sequence  
CC represents the amino acid sequence of ICM-1 binding humanised antibody  
CC domain. (Updated on 23-Oct-2003 to standardise OS field)  
XX  
XX  
SQ Sequence 116 AA;  
Query Match 98.9%; Score 610; DB 6; Length 116;  
Best Local Similarity 98.3%; Pred. No. 8.9e-47;  
Matches 114; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVDPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60  
DB 1 EVOLVESGGGLVDPGGSLRLSCAASGFINIKDTYIHWRQAPGKLEWVARIDPANDNTIY 60

QY 61 ADSVKGKFTTSSDSSKNTATYLONNSLRAEDTAVYYCTASGWPAYWGQGLTVTVSS 116  
DB 61 ADSVKGKFTTSSDSSKNTATYLONNSLRAEDTAVYYCTTSGWFPAYWGQGLTVTVSS 116

```

RESULT 6
ABO27259
ID ABO27259 standard; protein; 116 AA.
XX
AC ABO27259;
XX
DT 23-OCT-2003 (revised)
DT 11-SEP-2003 (first entry)
XX
DE ICM-1 binding humanised antibody Hunc VH domain.
XX
KW Human; mouse; ICM-1; intracellular adhesion molecule-1; bacteria;
KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
KW respiratory syncytial virus; fungi; antibody; humanised antibody.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
PN US2003035798-A1.
XX
PD 20-FEB-2003.
XX
PF 19-JUL-2001; 2001US-00910483.
XX
PR 30-NOV-1998; 98WO-US025422.
PR 16-AUG-2000; 2000US-0055446.
XX
PA (FANG/) FANG F.
PA (KOH/) KOHLSTAEDE L.
PA (RENO/) RENO J.
XX
PI Fang F, Kohlstaedt L, Reno J;
XX
DR WPI; 2003-503356/47.
XX
PT New humanized antibody binding ICM-1 and/or inhibits pathogen infection
PT of cells expressing ICM-1, useful for treating infection caused by HRV,
PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and
PT protozoa.
XX
PS Claim 1; Page 18; 30pp; English.
XX
CC The invention relates to a humanised antibody that binds intracellular
CC adhesion molecule-1, ICM-1 and/or inhibits pathogen infection of cells
CC expressing ICM-1, comprising any of the fully defined Huma to Humt
CC sequences. The methods and compositions are useful for inhibiting
CC infection and/or progression of infection caused by pathogens such as
CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,
CC bacteria, fungi and protozoa, in particular malaria. The present sequence
CC represents the amino acid sequence of ICM-1 binding humanised antibody
CC domain. (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 116 AA;
XX
Query Match 98.7%; Score 609; DB 6; Length 116;
Best Local Similarity 98.3%; Pred. No. 1,2e-46;
Matches 114; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 EVOLVESGGGLVPGGSLRLSCAASGFINIKDTYIHVWRQAPGKLEWVARIDPANDNTIY 60
Db 1 EVOLVESGGGLVPGGSLRLSCAASGFINIKDTYIHVWRQAPGKLEWVARIDPANDNTIY 60
XX
QY 61 ADSVKGKFTISSDPSKNTAYLQNSLRAEDTAIVYCTASGYWFAWGGTLVTYSS 116
Db 61 ADSVKGKFTISSDPSKNTAYLQNSLRAEDTAIVYCTASGYWFAWGGTLVTYSS 116
XX
RESULT 7
ABO27265
ID ABO27265 standard; protein; 117 AA.
XX
AC ABO27265;

```

```

XX
DT 23-OCT-2003 (revised)
DT 11-SEP-2003 (first entry)
XX
DE ICM-1 binding humanised antibody Humf VH domain.
XX
KW Human; mouse; ICM-1; intracellular adhesion molecule-1; bacteria;
KW human rhinovirus; human coxsackievirus; protozoa; malaria; infection;
KW respiratory syncytial virus; fungi; antibody; humanised antibody.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
PN US2003035798-A1.
XX
PD 20-FEB-2003.
XX
PF 19-JUL-2001; 2001US-00910483.
XX
PR 30-NOV-1998; 98WO-US025422.
PR 16-AUG-2000; 2000US-0055446.
XX
PA (FANG/) FANG F.
PA (KOH/) KOHLSTAEDE L.
PA (RENO/) RENO J.
XX
PI Fang F, Kohlstaedt L, Reno J;
XX
DR WPI; 2003-503356/47.
XX
PT New humanized antibody binding ICM-1 and/or inhibits pathogen infection
PT of cells expressing ICM-1, useful for treating infection caused by HRV,
PT coxsackie A virus, respiratory syncytial virus, bacteria, fungi and
PT protozoa.
XX
PS Claim 1; Page 19; 30pp; English.
XX
CC The invention relates to a humanised antibody that binds intracellular
CC adhesion molecule-1, ICM-1 and/or inhibits pathogen infection of cells
CC expressing ICM-1, comprising any of the fully defined Huma to Humt
CC sequences. The methods and compositions are useful for inhibiting
CC infection and/or progression of infection caused by pathogens such as
CC human rhinovirus, coxsackie A virus, respiratory syncytial virus,
CC bacteria, fungi and protozoa, in particular malaria. The present sequence
CC represents the amino acid sequence of ICM-1 binding humanised antibody
CC domain. (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 117 AA;
XX
Query Match 97.2%; Score 599.5; DB 6; Length 117;
Best Local Similarity 97.4%; Pred. No. 7,8e-46;
Matches 114; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
XX
QY 1 EVOLVESGGGLVPGGSLRLSCAASGFINIKDTYIHVWRQAPGKLEWVARIDPANDNTI 59
Db 1 EVOLVESGGGLVPGGSLRLSCAASGFINIKDTYIHVWRQAPGKLEWVARIDPANDNTI 60
XX
QY 60 YADSVKGRFTISSDPSKNTAYLQNSLRAEDTAIVYCTASGYWFAWGGTLVTYSS 116
Db 61 YADSVKGRFTISSDPSKNTAYLQNSLRAEDTAIVYCTASGYWFAWGGTLVTYSS 117
XX
RESULT 8
ABO27269
ID ABO27269 standard; protein; 116 AA.
XX
AC ABO27269;
XX
DT 23-OCT-2003 (revised)
DT 11-SEP-2003 (first entry)
XX
DE ICM-1 binding humanised antibody Humh VH domain.

```



XX Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;  
 KM human rhinovirus; human coxsackievirus; protozoa; malaria; infection;  
 KM respiratory syncytial virus; fungi; antibody; humanised antibody.  
 OS Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX US2003035798-A1.  
 XX 20-FEB-2003.  
 XX 19-JUL-2001; 2001US-00910483.  
 XX 30-NOV-1998; 98MO-US025422.  
 XX 16-AUG-2000; 2000US-00555446.  
 XX (FANG/) FANG F.  
 XX (KOH/) KOHLSTADT L.  
 XX (RENO/) RENO J.  
 XX Fang F, Kohlstaedt L, Reno J;  
 XX WPI; 2003-503356/47.  
 XX New humanized antibody binding ICAM-1 and/or inhibits pathogen infection  
 PT of cells expressing ICAM-1, useful for treating infection caused by HRV,  
 PT coxackie A virus, respiratory syncytial virus, bacteria, fungi and  
 PT protozoa.  
 XX Claim 1; Page 19; 30pp; English.  
 XX The invention relates to a humanised antibody that binds intracellular  
 CC adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells  
 CC expressing ICAM-1, comprising any of the fully defined Huma to Humi  
 CC sequences. The methods and compositions are useful for inhibiting  
 CC infection and/or progression of infection caused by pathogens such as  
 CC human rhinovirus, coxackie A virus, respiratory syncytial virus,  
 CC bacteria, fungi and protozoa, in particular malaria. The present sequence  
 CC represents the amino acid sequence of ICAM-1 binding humanised antibody  
 CC domain. (Updated on 23-OCT-2003 to standardise OS field)  
 XX  
 XX Sequence 116 AA:  
 SQ  
 Query Match 95.5%; Score 589; DB 6; Length 116;  
 Best Local Similarity 94.8%; Pred. No. 6.6e-45;  
 Matches 110; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYTHWVROAPGKLEWVARIDPANDNTIY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYTHWVROAPGKLEWVARIDPANDNTIY 60  
 QY 61 ADSYKGRFTISDDSKNTAYLQNNSLRAEDTAVYYCTASGYWFAWVGGLVTYSS 116  
 DB 61 DPKYQGRFTISADSKNTAYLQNNSLRAEDTAVYYCTTSGWFAWVGGLVTYSS 116  
 RESULT 9  
 ID ABO27263 standard; protein; 116 AA.  
 AC ABO27263;  
 XX  
 DT 23-OCT-2003 (revised)  
 DT 11-SEP-2003 (first entry)  
 XX  
 DE ICAM-1 binding humanised antibody Hume VH domain.  
 XX Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;  
 KM human rhinovirus; human coxsackievirus; protozoa; malaria; infection;  
 KM respiratory syncytial virus; fungi; antibody; humanised antibody.  
 XX

OS Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX US2003035798-A1.  
 XX 20-FEB-2003.  
 XX 19-JUL-2001; 2001US-00910483.  
 XX 30-NOV-1998; 98MO-US025422.  
 XX 16-AUG-2000; 2000US-00555446.  
 XX (FANG/) FANG F.  
 XX (KOH/) KOHLSTADT L.  
 XX (RENO/) RENO J.  
 XX Fang F, Kohlstaedt L, Reno J;  
 XX WPI; 2003-503356/47.  
 XX New humanized antibody binding ICAM-1 and/or inhibits pathogen infection  
 PT of cells expressing ICAM-1, useful for treating infection caused by HRV,  
 PT coxackie A virus, respiratory syncytial virus, bacteria, fungi and  
 PT protozoa.  
 XX Claim 1; Page 18; 30pp; English.  
 XX The invention relates to a humanised antibody that binds intracellular  
 CC adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells  
 CC expressing ICAM-1, comprising any of the fully defined Huma to Humi  
 CC sequences. The methods and compositions are useful for inhibiting  
 CC infection and/or progression of infection caused by pathogens such as  
 CC human rhinovirus, coxackie A virus, respiratory syncytial virus,  
 CC bacteria, fungi and protozoa, in particular malaria. The present sequence  
 CC represents the amino acid sequence of ICAM-1 binding humanised antibody  
 CC domain. (Updated on 23-OCT-2003 to standardise OS field)  
 XX  
 XX Sequence 116 AA:  
 SQ  
 Query Match 95.5%; Score 589; DB 6; Length 116;  
 Best Local Similarity 94.8%; Pred. No. 6.6e-45;  
 Matches 110; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYTHWVROAPGKLEWVARIDPANDNTIY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFINIKDTYTHWVROAPGKLEWVARIDPANDNTIY 60  
 QY 61 ADSYKGRFTISDDSKNTAYLQNNSLRAEDTAVYYCTASGYWFAWVGGLVTYSS 116  
 DB 61 DPKYQGRFTISADSKNTAYLQNNSLRAEDTAVYYCTTSGWFAWVGGLVTYSS 116  
 RESULT 10  
 ID ABO27271 standard; protein; 116 AA.  
 AC ABO27271;  
 XX  
 DT 23-OCT-2003 (revised)  
 DT 11-SEP-2003 (first entry)  
 XX  
 DE ICAM-1 binding humanised antibody Humi VH domain.  
 XX Human; mouse; ICAM-1; intracellular adhesion molecule-1; bacteria;  
 KM human rhinovirus; human coxsackievirus; protozoa; malaria; infection;  
 KM respiratory syncytial virus; fungi; antibody; humanised antibody.  
 XX Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX US2003035798-A1.  
 XX

XX 20-FEB-2003.  
PD ABR55857  
XX 19-JUN-2001; 2001US-00910483.  
PE 30-NOV-1998; 98WO-US025422.  
XX 16-AUG-2000; 2000US-00555446.  
PR  
XX (FANG/) FANG F.  
PA (KOHL/) KOHLSTADT L.  
XX (RENO/) RENO J.  
XX Fang F, Kohlstaedt L, Reno J;  
PI WPI; 2003-503356/47.  
XX  
XX New humanized antibody binding ICAM-1 and/or inhibits pathogen infection  
PT of cells expressing ICAM-1, useful for treating infection caused by HIV,  
PT coxackie A virus, respiratory syncytial virus, bacteria, fungi and  
PT protozoa.  
XX  
XX Claim 1; Page 20; 30pp; English.  
XX  
XX The invention relates to a humanised antibody that binds intracellular  
CC adhesion molecule-1, ICAM-1 and/or inhibits pathogen infection of cells  
CC expressing ICAM-1, comprising any of the fully defined Huma to Humt  
CC sequences. The methods and compositions are useful for inhibiting  
CC infection and/or progression of infection caused by pathogens such as  
CC human rhinovirus, coxackie A virus, respiratory syncytial virus,  
CC bacteria, fungi and protozoa, in particular malaria. The present sequence  
CC represents the amino acid sequence of ICAM-1 binding humanised antibody  
CC domain. (Updated on 23-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 116 AA:

Query Match 93.4%; Score 576; DB 6; Length 116;  
Best Local Similarity 92.2%; Pred. No. 9.5e-44;  
Matches 107; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVPGGSLRLSCAASGFRNIKDTYIHWVRQAPGKGLEWVARIDPANDNTIY 60  
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFRNIKDTYIHWVRQAPGKGLEWVARIDPANDNTIY 60  
QY 61 ADSVKGRFTTSSDSSKNTAYLQWNSLRAPDTAVYYCTASGTFWYWGQGLTVTVSS 116  
DB 61 DPKYQGRFTMSADTSSKNTAYLQWNSLRAPDTAVYYCTTSGWTFWYWGQGLTVTVSS 116  
RESULT 11  
ID ABR55857 standard; protein; 120 AA.  
XX ABR55857;  
AC ABR55857;  
XX  
DT 02-SEP-2003 (first entry)  
XX  
DE Anti-Her-2 Mab herceptin heavy chain.  
XX  
KW Peptide remodeling; glycoconjugation; glycosyltransferase; glycan;  
KW antibody; Her-2; epidermal growth factor receptor.  
XX  
OS Mus musculus.  
XX  
XX WO2003031464-A2.  
XX  
PD 17-APR-2003.  
XX  
PF 09-OCT-2002; 2002WO-US032263.  
XX  
PR 10-OCT-2001; 2001US-0328523P.  
PR 19-OCT-2001; 2001US-0344692P.  
PR 28-NOV-2001; 2001US-0334233P.  
PR 28-NOV-2001; 2001US-0334301P.

PR 07-JUN-2002; 2002US-0387292P.  
PR 25-JUN-2002; 2002US-0391777P.  
PR 17-JUN-2002; 2002US-0396594P.  
PR 16-AUG-2002; 2002US-0404249P.  
PR 28-AUG-2002; 2002US-0407527P.  
XX  
XX (NEOS-) NEOSE TECHNOLOGIES INC.  
XX  
XX De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;  
PI WPI; 2003-449162/42.  
XX  
XX  
XX Remodeling a peptide, by removing a saccharyl subunit from the peptide to  
PT form truncated glycan, and adding or deleting glycosyl groups to a  
PT peptide and/or adding modifying group of a peptide to remodel the  
PT peptide.  
XX  
XX Example; Fig 72B; 900pp; English.

XX The invention relates to a cell-free, in vitro method of remodeling a  
CC peptide. The method involves removing a saccharyl subunit from the  
CC peptide, thus forming a truncated glycan, and contacting the truncated  
CC glycan with at least one glycosyltransferase and at least one glycosyl  
CC donor under conditions suitable to transfer at least one glycosyl donor  
CC to the truncated glycan, thus remodeling the peptide. Conjugates can be  
CC formed between a granulocyte colony stimulating factor (G-CSF) peptide,  
CC interferon alpha peptide, interferon beta peptide, Factor VIIa peptide,  
CC Factor IX peptide, follicle stimulating hormone peptide, erythropoietin  
CC (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF)  
CC peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-P1)  
CC peptide, beta-glucosidase peptide, tissue plasminogen activator (tPA)  
CC peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha  
CC receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-  
CC glycoprotein IIB/IIIA monoclonal antibody peptide, chimeric anti-HER2  
CC antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-  
CC CD20 antibody peptide, recombinant DNase peptide, anti-TNF alpha peptide,  
CC insulin peptide, hepatitis B surface antigen (HbsAg), human growth  
CC hormone (HGH) peptide, and a modifying group, where the modifying group  
CC is covalently attached to the peptide through an intact glycosyl linking  
CC group. The method is useful for a cell-free, in vitro method of  
CC remodeling the above mentioned peptides. The present sequence represents  
CC an anti-Her-2 (human epidermal growth factor receptor) Mab herceptin  
CC heavy chain  
XX

SQ Sequence 120 AA:  
Query Match 84.0%; Score 518; DB 6; Length 120;  
Best Local Similarity 85.8%; Pred. No. 1.4e-38;  
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCAASGFRNIKDTYIHWVRQAPGKGLEWVARIDPANDNTIY 60  
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFRNIKDTYIHWVRQAPGKGLEWVARITVNGTTRY 60  
QY 61 ADSVKGRFTTSSDSSKNTAYLQWNSLRAPDTAVYYCTASG---YWFAYWGQGLTVTVSS 116  
DB 61 ADSVKGRFTTSSDSSKNTAYLQWNSLRAPDTAVYYCSRWGSGDFYANDYWGQGLTVTVSS 120  
RESULT 12  
ID ADD35374 standard; protein; 120 AA.  
XX ADD35374;  
AC ADD35374;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human MAb4D5-8 heavy chain variable domain SEQ ID NO:2.  
XX  
KW antibody heavy chain variable domain; hypervariable region; HER2 binding;  
KW humanised anti-HER2 antibody; cytostatic; antiinflammatory;  
KW immunosuppressive; gene therapy; cancer; breast cancer; tumour;  
KW leukaemia; lymphoid malignancy.

XX OS Homo sapiens.  
XX PN MO2003087131-A2.  
XX PD 23-OCT-2003.  
XX PF 09-APR-2003; 2003WO-US011031.  
XX PR 10-APR-2002; 2002US-0371609P.  
XX PA (GETH ) GENENTECH INC.  
XX PI Lowman HB, Gershten RB, Carter PJ;  
XX WPI; 2003-845297/78.  
XX  
XX PT New polypeptide comprising an antibody light or heavy chain variable  
XX PT variants, specifically anti-HER2 antibody variants, useful for treating  
XX PT cancer, tumor, inflammatory, immunologic or angiogenic disorders.  
XX  
XX PS Claim 14; SEQ ID NO 2; 96pp; English.  
XX  
XX CC The present invention describes a polypeptide (I) comprising an antibody  
XX CC light chain variable domain having hypervariable regions of a sequence of  
XX CC 109 amino acids (P1, seeADJ3573), where one or more amino acids selected  
XX CC from Q27(VL), D28(VL), N30(VL), T31(VL), A32(VL), Y49(VL), F53(VL),  
XX CC Y55(VL), R66(VL), H91(VL), Y92(VL), and T94(VL), numbered according to  
XX CC the Kabat numbering system, are substituted with any amino acid other  
XX CC than alanine. Also described: (1) an antibody that is capable of binding  
XX CC to the extracellular domain of HER2, which comprises the hypervariable  
XX CC regions P1 and/or P2 (see ADJ3574); (2) a humanised anti-HER2 antibody  
XX CC comprising one or more of the substitutions described above; (3) an  
XX CC article of manufacture comprising a container, a composition contained in  
XX CC it, and a package insert or label indicating that the composition can be  
XX CC used to treat cancer characterised by the overexpression of HER2, where  
XX CC the composition comprises the antibody described above; (4) an antibody  
XX CC variant of a parent antibody which binds HER2, comprising an amino acid  
XX CC substitution at position 98 of its heavy chain variable domain, and where  
XX CC the binding affinity of the antibody variant for HER2 is better than the  
XX CC binding affinity of the parent antibody for HER2; and (5) isolating high-  
XX CC affinity variants of humanised anti-HER2 antibody. (1) has cytostatic,  
XX CC antiinflammatory and immunosuppressive activities, and can be used in  
XX CC gene therapy. The polypeptide and compositions are useful for treating  
XX CC cancer, e.g. breast cancer, benign or malignant tumours, leukaemias and  
XX CC lymphoid malignancies, and other disorders such as neural, glial,  
XX CC astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal,  
XX CC blastocoealic, inflammatory, angiogenic, and immunologic disorders. The  
XX CC present sequence represent the heavy chain variable domain of humAb4D5-8,  
XX CC which is used in the exemplification of the present invention.  
XX  
XX SQ Sequence 120 AA;  
XX  
XX Query Match 84.0%; Score 518; DB 7; Length 120;  
XX Best Local Similarity 85.8%; Pred. No. 1.4e-38;  
XX Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;  
XX  
XX QY 1 EVQLVESGGGLVOPGSGLRISCAASGFNIKDTYIHMYRQAPGKLEWVARIDPANDNTIY 60  
XX DB 1 EVQLVESGGGLVOPGSGLRISCAASGFNIKDTYIHMYRQAPGKLEWVARIPYNGTRY 60  
XX  
XX QY 61 ADSYKGRFTISDDSKNTAYLQNNSLRAEDPAVYYCTASG----YWPAYWGQGLTVTVSS 116  
XX DB 61 ADSYKGRFTISADTSKNTAYLQNNSLRAEDPAVYYCSRWGSDGYANDYWGQGLTVTVSS 120  
XX  
XX RESULT 13  
XX ADC26167 standard; protein, 228 AA.  
XX AC ADC26167;  
XX DT 18-DEC-2003 (first entry)

XX DE Humanised anti-HER2 antibody 4D5 heavy chain variable domain protein.  
XX KM antibody variant; cytostatic; cancer; heavy chain variable domain; 4D5;  
XX KM anti-HER2; human.  
XX OS Unidentified.  
XX OS Homo sapiens.  
XX PN MO2003068801-A2.  
XX PD 21-AUG-2003.  
XX PF 11-FEB-2003; 2003WO-US004184.  
XX PR 11-FEB-2002; 2002US-0355895P.  
XX PR 10-SEP-2002; 2002US-0409685P.  
XX PA (GETH ) GENENTECH INC.  
XX PI Lowman HB, Marvin JS;  
XX WPI; 2003-697521/66.  
XX  
XX PT Making an antibody variant of a parent antibody specific to an antigen by  
XX PT identifying a target amino acid residue within the variable domain of the  
XX PT parent antibody and substituting the target residue with a different  
XX PT amino acid residue.  
XX  
XX PS Claim 35; SEQ ID NO 14; 81pp; English.  
XX  
XX CC The invention relates to a novel method for making an antibody variant of  
XX CC a parent antibody specific to an antigen. This is achieved via  
XX CC identifying a target amino acid residue within the variable domain of the  
XX CC parent antibody and substituting the target residue with a different  
XX CC replacement amino acid residue such that the charge complementarity  
XX CC between the antibody and antigen is increased. The antibody variant of  
XX CC the invention demonstrates cytostatic activity whilst the method may be  
XX CC useful for treating cancer. The current sequence is that of the humanised  
XX CC anti-HER2 antibody 4D5 heavy chain variable domain protein of the  
XX CC invention.  
XX  
XX SQ Sequence 228 AA;  
XX  
XX Query Match 84.0%; Score 518; DB 7; Length 228;  
XX Best Local Similarity 85.8%; Pred. No. 2.8e-38;  
XX Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;  
XX  
XX QY 1 EVQLVESGGGLVOPGSGLRISCAASGFNIKDTYIHMYRQAPGKLEWVARIDPANDNTIY 60  
XX DB 1 EVQLVESGGGLVOPGSGLRISCAASGFNIKDTYIHMYRQAPGKLEWVARIPYNGTRY 60  
XX  
XX QY 61 ADSYKGRFTISDDSKNTAYLQNNSLRAEDPAVYYCTASG----YWPAYWGQGLTVTVSS 116  
XX DB 61 ADSYKGRFTISADTSKNTAYLQNNSLRAEDPAVYYCSRWGSDGYANDYWGQGLTVTVSS 120  
XX  
XX RESULT 14  
XX AAB28158  
XX ID AAB28158 standard; protein, 252 AA.  
XX AC AAB28158;  
XX DT 08-FEB-2001 (first entry)  
XX DE Human anti-c-ErbB2 single chain Fv fragment 4D5.  
XX KM Human; immunoglobulin; antigen-binding; framework region; carcinoma;  
XX KM c-ErbB2; carcinoma-associated antigen.  
XX OS Homo sapiens.  
XX PN MO200061635-A2.

XX 19-OCT-2000.  
PD  
XX  
PF 10-APR-2000; 2000MO-EP003176.  
XX  
PR 09-APR-1999; 99EP-00107030.  
XX  
PA (UYZU-) UNIV ZUERICH.  
XX (PLUE/) PLUECKTHUN A.  
XX  
PI Plueckthun A, Honegger A, Willuda J;  
DR WPI; 2000-679468/66.  
XX  
PT Stabilizing chimeric immunoglobulin (Ig) involves setting up a stabilized  
PT antigen binding Ig or its fragment by replacing one or more residues  
PT present in acceptor Ig by those residues present in donor Ig.  
XX  
PS Claim 5; Page 51; 51pp; English.  
XX  
CC The present invention relates to a method for stabilizing a chimeric  
CC immunoglobulin (Ig). The method comprises identifying antigen-binding  
CC groups derived from donor Ig and framework regions derived from an  
CC acceptor Ig. The present sequence is one such acceptor Ig fragment. One  
CC or more of the residues present at the positions in the present sequence  
CC are replaced by those present at the corresponding positions in the donor  
CC Ig, after comparing the structural features of the VH domains of the  
CC acceptor Ig and the donor Ig. The method of the present invention is  
CC useful for producing a pharmaceutical composition which can be used for  
CC treating human carcinomas, since c-erbB2 is a carcinoma-associated  
CC antigen  
CC  
SQ Sequence 252 AA;  
  
Query Match 84.0%; Score 518; DB 3; Length 252;  
Best Local Similarity 85.8%; Pred. No. 3.7e-38;  
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;  
  
QY 1 EVOLVESGGGLVQPGGSLRLSCAASGPNIKDTYTHWRQAPGKGLEWVARIDPANDNTIY 60  
DB 133 EVOLVESGGGLVQPGGSLRLSCAASGPNIKDTYTHWRQAPGKGLEWVARIYPNGYTRY 192  
  
QY 61 ADSVKGKFTTSSDSSKNTAYLQWNSLRAEDTAVYYCTASG---YMPAYWGQGLTVTVSS 116  
DB 193 ADSVKGKFTTSSDSSKNTAYLQWNSLRAEDTAVYYCSRWGDDGFYANDYWGQGLTVTVSS 252  
  
RESULT 15  
ADBS5320  
ID ADB85320 standard; protein; 449 AA.  
XX  
AC ADB85320;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Heavy chain of the humanised anti-HER2 antibody, Herceptin/Trastuzumab.  
XX  
KM CH2/CH2; protein A chromatography; protein purification; antibody; HER-2;  
KM Herceptin; Trastuzumab; heavy chain.  
XX  
OS Synthetic.  
XX Unidentified.  
XX  
PN US2003153735-A1.  
XX  
PD 14-AUG-2003.  
XX  
PF 03-FEB-2003; 2003US-00356974.  
XX  
PR 05-FEB-2002; 2002US-0354579P.  
XX  
PA (GETH) GENENTECH INC.  
XX

PI Breese TN, Fahrner RL, Gorrell JR, Lazareschi KP, Lester PM;  
PI Peng D;  
XX  
DR WPI; 2003-678834/64.  
XX  
PT Purifying proteins by Protein A chromatography without using toxic  
PT chemicals, comprises removing contaminants by washing the solid phase  
PT with intermediate buffers e.g. detergent and salt.  
XX  
PS Disclosure; Fig 1B; 24pp; English.  
XX  
XX The invention relates to purifying a protein, which comprises a CH2/CH2  
CC region, from a contaminated solution by Protein A chromatography  
CC comprising: (1) adsorbing the protein to immobilized Protein A; (2)  
CC removing contaminants by washing the solid phase with a composition  
CC comprising: (a) detergent and salt; (b) a buffer at a concentration  
CC greater than 0.8 M; (c) salt and solvent; or (d) salt and a polymer; and  
CC (3) recovering the protein from the solid phase. The method is used to  
CC purify proteins, especially anti-HER (e.g. Herceptin/Trastuzumab) and  
CC anti-IGF antibodies and immunoadhesins. The intermediate wash buffers  
CC used remove contaminants without removing significant amounts of the  
CC protein of interest bound to Protein A. In addition the methods avoid the  
CC use of prior art chemicals such as tetramethylammonium chloride which is  
CC difficult to handle and dispense, toxic, requires costly disposal as  
CC hazardous waste and is corrosive at high concentration and low pH. The  
CC present sequence is the heavy chain of the humanised anti-HER2 antibody,  
CC Herceptin/Trastuzumab.  
XX  
SQ Sequence 449 AA;  
  
Query Match 84.0%; Score 518; DB 7; Length 449;  
Best Local Similarity 85.8%; Pred. No. 5.7e-38;  
Matches 103; Conservative 2; Mismatches 11; Indels 4; Gaps 1;  
  
QY 1 EVOLVESGGGLVQPGGSLRLSCAASGPNIKDTYTHWRQAPGKGLEWVARIDPANDNTIY 60  
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGPNIKDTYTHWRQAPGKGLEWVARIYPNGYTRY 60  
  
QY 61 ADSVKGKFTTSSDSSKNTAYLQWNSLRAEDTAVYYCTASG---YMPAYWGQGLTVTVSS 116  
DB 61 ADSVKGKFTTSSDSSKNTAYLQWNSLRAEDTAVYYCSRWGDDGFYANDYWGQGLTVTVSS 120  
  
Search completed: May 13, 2004, 16:56:28  
Job time : 139.125 secs